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					SUMMARIES		
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ALIGNMENTS

RESULT 1

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	2705 bp mRNA linear PLN 03-OCT-2001	e cds.						Tracheophyta	Ginkgo.			imaradiene	n ginkgolide
	linear	nRNA, complet						Embryophyta;	Ginkgoaceae;			biloba levopi	itted step ir
	p mRNA	synthase 1				_		ptophyta;	nkgoales;		t Buda, S.P	f Ginkgo	irst comm
	2705 bj	vopimaradiene		5865604		aidenhair tree		iplantae; Stre	inkgophyta; Gi	705)	Pang, J. and Ma	acterization o	stalyzes the f
	AF331704	DEFINITION Ginkgo biloba levopimaradiene synthase mRNA, complete cds.	AF331704	AF331704.1 GI:15865604		Ginkgo biloba (maidenhair tree)	Ginkgo biloba	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.	1 (bases 1 to 2705)	Schepmann, H.G., Pang, J. and Matsuda, S.P.	Cloning and chara	synthase which catalyzes the first committed step in ginkgolide
AF331704	rocus	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

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BEBEALGHYGIIDMLKELNWELANPEANNFALVORRLINDKTYQAERNRGELVSSVQCYMRENPECT
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Schepmann, H.G. and Matsuda, S.P.T.
Schepmann, H.G. and Matsuda, S.P.T.
Direct Submission
Submitted (21-D200) Chemistry, Rice University, 6100
Street, Houston, TX 77005, USA
Location/Qualifiers
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/protein_id="AAL09965.1"
/db_xref="G1:18865605"
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100.0%; Score 2705;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2705; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:3311"
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Methods of making modified polypeptides
Patent: US 6468772-A 55 22-0CT-2002;
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                          2570 AGAGATGGCTITGCTATCTC---TGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTT
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                        ATCGACAACGCACTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGCGAGCAATGCCCCA
                                                                                                                                                                      TTGTGTGTGAGAAGACTGCTGTTCAACACTGCAAGAGTGCAGCTGTTTTATATGTAC
   GACACCAAGACTTACCAGGCCGAGAGAAACCGTGGTGAATTGGTTTCCAGCGTACAGTGC
                                                                          TACATGAGGGAAAATCCGGAGTGCACAGAGGAAGAAGCTCTAAGTCATGTTTATGGTATC
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Unclassified.
I (bases 1 to 2861)
Chappell, J., Manna, K.R., Noel, J.P. and St. Synthases
AL Patent: US 6495354-A 55 17-DEC-2002;
Location/Qualifiers
Al Patent: Al Patent: Al Patent Al Pa
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Sequence 55 from patent US 6495354.
AR266986

    2861
    /organism="unknown"
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Best Local Similarity 68.4%;
Matches 1574; Conservative
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                                                                                 Length 2861;
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                                                                               Similarity 68.4%; Pred. No. 3e-291;
4; Conservative 0; Mismatches 713;
    06-MAY-2003;
 : US 6559297-A 55 06-MAY-20
Location/Qualifiers
1. .2861
/organism="unknown"
/mol_type="genomic DNA"
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GTGACGGAAATATTTCTCACCGGCATCCTTTATCTTTGAGCCCGAGTTTTCTAAGTGC 1820
                                  AGAATTGCCTATGCCAAGACTTCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACACC 1909
                                                  CGAAAAGTATGGGAGGGCTTGCTCGCATCGTATACCAAAGAAGCCGAATGGTCGGCAGCA 2149
                                                                                                                                                                                                                               AAGTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCCATAGCACTTGCG 2209
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                                                                                                                                                 CTAGTGGA---CCAAATGCCACAAATGAAATATGTTTTTGTGGGTTTCTACAATACT 1997
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                                                                                                                          GTGCTGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTACAACACA
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Unclassified.
1 (bases 1 to 2861)
Chappell.J., Manna,K.R., Noel,J.P. and Starks,C.M.
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Sequence 55 from patent US 6559297.
AR316335.1 GI:31711070
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                                                                                               TTGTGTGTGAGAAGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATGTAC
                                                                                                             350 GICGATGAGAATCAATAAAAGAATCCAGACATTGGTGAAAGGAAATCCAGTGCATGTTT
                                                                       Arggaaaarcccrcgaagacrrgaaraggagrrrgrgaa-----raacaaaaraccg
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                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 2861)

1 (bases 1, Manna, K.R., Noel, J.P. and Starks, C.M. Synthaesl, J., Manna, K.R., Noel, J.P. and Starks, C.M. Synthaest, J. Manna, K.R., S. 27-MAY-2003;
        TACATGAGGAAAATCCGGAGTGCACAGAGGAAGAAGCT
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Sequence 55 from patent US 6569656.
AR338478
AR338478.1 GI:33725255
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1. .2861
/organism="unknown"
/mol_type="genomic DNA"
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804 GCTAAGCTIAAAAGGATICCCACGATGTICTCTATGCCCTICCAACAACGTTAITGTAT 863 409 383 469 443 529 503 589 563 649 623 GIGCAGAAAGGGGITGAGIIIGIGAGAAAACACAIGGAAGAAATGAAGGAGGAGGTGAC 709 683 AATCACAGGCCAAGTGGATTCGAGGTCGTGTTTCCTGCAATGTTAGATGAAGCAAAAAGC 769 743 829 803 AAACGAŢĠĊĊŢĊĊŖĊŢŢŢĊŢŢĊĠŢĠĊŢĊŖĠĊŖĀAŢŢŢĠĠĊĠĄĊŢĀĊĠŢŢĊĊŢŢĠĊ ATCGATCGCTATTTCAAGAAAGAAATCAAAGAATCTCTGGATTACGTTTATAGGTACTGG s64 aracitegenacaritecarenararrakecerracerregegaraeregegagaeacaaa 624 GTACAGAAAGGTATTGAATTCTTCAGGACACAAGCTGGAAAGATGGAAGATGAAGCTGAT TIGGGATIGGATCTICCTIATCACCICCCTITCATCTCCCAAAATCCACAAAAGCGCCAG GTTGCAGCATCAGACGAGAAGCGTATCGAGACATTAATATCCGAGATTAAGAATATGTTT CAGTCCATGGGCGACGGTGAAACGAATCCATCTGCATATGATACAGCTTGGGTGGCAAGA AGATGTATGGGCTATGGCGAAACGAATCCCTCTGCATATGACACTGCTTGGGTAGCAAGG ATTCCGTCAATTGACGGCTCTGGTGCACCCCAATTTCCCCCAAACGCTTCAATGGATTCTG AACAATCAACTGCCAGATGGCTCGTGGGGTGAGGAGTGCATTTTTCTGGCGTATGACAGA GTCGATGAGACAATCAATAAAAGAATCCAGACATTGGTGAAGGAAATCCAGTGCATGTTT Сарв 15; Length 2861; Indels 40.3%; Score 1091.4; DB 6; .larity 68.4%; Pred. No. 3e-291; Conservative 0; Mismatches 713;] /organism="unknown" /mol_type="genomic DNA' Best Local Similarity Matches 1574; Conser 924 1010 1070 1044 1130 1190 1164 1250 1104 950 350 384 444 530 504 590 650 710 770 410 324 Query Match ORIGIN 8 8 8 8 6 B 6 B 6 B 6 \$ B \$ B \$ B \$ B \$ B 8 & 8 g 8 & ያ ያ

2329 2389 2117 2297 TACATGAGGAAAATCCGGAGTGCACAGAGAAGAAGCTCTAAGTCATGTTATGGTATC 2449 2149 AAGTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCG 2209 2177 1609 1669 1640 1729 1700 1789 1880 1969 2029 2089 2057 2178 ACAGICGITCICATIAGIGCICTITICACIGGGAGGATCITACAGAIGAAGIACICICC 2237 1400 1520 1580 CCTGTGGAAATGTATTTCTCAGTGGCGGTTAGTATGTTTGAGCCAGAATTCGCTGCTTGT 1849 GTGACGGAAATATATTTCTCACCGGCATCCTTTATCTTTGAGCCCGGGTTTTCTAAGTGC 1820 AGAATTGCCTATGCCAAGACTTCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACGC 1909 2210 ACAGTCGTACTAAACTCCAATCTTTTCACTGGAGAATTACTTCCTGATTACATTTTACAG GTGCTGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTACAACACA 1998 TTTAATGATATAGCAAAAGAAGGACGTGAGAGGCCAAGGGCGCGATGTGCTAGGCTACATT CGAAAAGTATGGGAGGGCTTGCTCGCATCGTATACCAAAGAAGCCGAATGGTCGGCAGCA 2270 CAAGTAGACCTTCGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTAATCAAT CACGGATCTCTGGATGATCTTGATTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCT 2030 GIGAAIGGATTIGGAAAAGAIGGACTCAAGGAACAAGGCCGTGAIGTGCTGGGCTAICTT AATGATGTCTGGCTGGGGAAGACTGTGTTAAGATGCTATATGTGAGCAACGAAAATAT GAAGAAGCTAAAGACCTTCACTACAATCATCTCCCAAAATGCTCTTGCCAAAAAAAGAA ccraccataagagtatgccaaggttggaggctagaagctatattgaaaactatggggcca TTGGAGCTGGCCAAATTGGACTTCAATATGGTGCAGGCCTTACACCAAAAGGAGACTCAA CACATIGICAGCIGGAGAGAATCGGGATICAATGATCTTACATTCACCGGCCAGGG **ACCGATAATCTTAACCTTTATAGATGTTCACAAGTATGTTTTCCGGGAGAAAAGATAATG** TTTGATAAGTGGGCTGTCAAGAAGGATCTTCCTGGAGAGGTGGAGTATGCTATAAAGTAT 2330 2150 2238 2390 1790 2090 2058 1610 1641 1730 1850 1821 1881 1970 1490 1581 1670 1701 1461 1550 1521 1761 1281 1430 1401 g 요 8 8 දු පු ⋧ 셤 ò 원 장 8 6 B 6 B 6 B 6 B 6 B 8 & 8 ò 8 S ò 쉽 8 g 8 8 S

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LYLRWGKGSRKIIACVGBGGATSVPYQSABKNDSLSSSTLVKKBFPPCFWKDDLIDSL
TSSHKVAASDEKRIETLISEIKNMFRCMGGTENDESAYDTAWVARIPAVDBLIDSL
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GWARRHPVPCHYPCHYPLLYSTRANTSTROMGEFFCFLGGTGRGYDBL
NVRRCSHVSFPGITJMERAKLCTERYLRANALBNVDAPDKWAFKGNIRGSVEYALKYPW
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DLARWWKSSGFTDLAPTREAVTEITYPPAMLKTVPHYPUSDLY
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DAHGSLDDLKLFTESVKRWDLSLVDQMPQQMKICFVGFYNTFNDIAKEGFREYCKDVL
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Abies grandis abietadiene synthase (ac22) mRNA, complete cds.
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DEVLSKIDRESRFLOLMGLTGRLVNDTKTYQAERGQGEVASAIOCYMKOHPKISBEBA
LQHYSVMERALBELMREFVNNKIPDIYKRLVPETARIMQLFYMQGDGLTLSHDMBIK
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
1 (bases 1 to 2861)
Stoffer-Vogel, B., Wildung, M.R., Vogel, G. and Croteau, R.B.
Direct Submission
Submitted (106-MAR-1996) Mark Wildung, IBC, Washington State
University, Pullman, WA 99164-6340, USA
TATATGAAGGACCATCCTAAAATCTCTGAAGAAGAAGCTCTACAACATGTCTATAGTGTC
                                ATCGACAACGCACTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGCGAGCAATGCCCCA
                                                                                             TTGTGTGTGAGAAGACTGCTGCTACACACAGAGAGTGATGCAGCTGTTTTATATGTAC
                                                            ATGGAAAATGCCCTCGAAGAGTTGAATAGGGAGTTTGTGAA-----TAACAAAATACCG
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/product="abletadiene cyclase"
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                                                                                    CAGTCCATGGGCGACGGTGAACGAATCCATCTGCATATGATACAGCTTGGGTGGCAAGA
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Best Local Similarity 59.7%; Pred. No. 2.3e-191;
Matches 1369; Conservative 0; Mismatches 894;
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Sequence 39 from patent US 6451576.
AR230308. GI:27270431
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/organism="unknown"
/mol_type="genomic DNA"
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Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
Synthases
Patent: JP 2002526066-A 23 20-AUG-2002;
UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR SEIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES
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PN JP 2002526066-A/23
PD 20-AUG-2002
PP 17-SEP-1999 JP 2000574228
PR 18-SEP-1999 US 60/130628
23-AUG-1999 US 60/150262
PI JOSEPH CHAPPELL, KATHLEEN R MANNA, JOSEPH P NOEL, COURTNEY ISTARKS
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/organism="Abies grandis"
/mol_type="genomic DNA"
/db_xref="taxon:46611"
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                                                          AAATTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTGGATAGCGTTCGGGAT
                                                                      TAT---ATGAAACTATGTTACCAAATCTATTATGACATAGTTCACGAGGTGGCTTGGGAG
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              AAATTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTGGATAGCGTTCGGGAT
                                                       GGACTCAAGGAACAAGGCCGTGATGTGCTGGCTATCTTCGAAAAGTATGGGAGGGCTTG
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                               GACCTGCCTTATATACATCTGTTGCAGACTAAACGGCAGGAAGATTAGCAAAACTTTCA
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                                                          Query Match 27.0%; Score 730.2; DB 6; Best Local Similarity 59.6%; Pred. No. 5.6e-191; Matches 1370; Conservative 0; Mismatches 893;
Chappell, J., Manna, K.R., Noel, J.P. and
Synthases
Patent: US 6495354-A 45 17-DEC-2002;
Location/Qualifiers
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Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
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L Patent: US 6559297-A 45 06-MAY-2003;
Location/Qualifiers
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RESULT
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(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaa38937 Grand fir	Aax87530 E-alpha-b	Aax08654 Grand Fir	Aaa38932 Grand fir	Aaf73382 Grand fir	Aax87529 Grand fir	Aax87531 E-alpha-b	Aax87504 Grand fir	Aat97447 Pacific y	1 Yew ta	~	Aaf73421 Grand fir	-	Aaf73391 Grand fir	Aaa38933 Grand fir	Aax87532 Delta-sel	4	Aax87533 Delta-sel	Aax87505 Grand fir		Aaa38927 Grand fir	Aaf73371 Grand fir	Aaz99415 Spybean c
SUMMARIES	;	aı	AAA38937	AAX87530	AAX08654	AAA38932	AAF73382	AAX87529	AAX87531	AAX87504	AAT97447	AAA38931	AAF73412	AAF73421	AAX08663	AAF73391	AAA38933	AAX87532	AAX87534	AAX87533	AAX87505	AAX08643	AAA38927	AAF73371	AAZ99415
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	Query	Match	40.3	27.0	27.0	27.0	27.0	27.0	27.0	27.0	23.7	23.7	16.7	15.4	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.1
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AAD40203	AAX08645	AAA38938	AAF73373	AAX87513	AAX08655	AAF73383	AAX08644	AAA38922	AAF73372	AAF73413	AAT15761	AAA69551	AAA69644	AAF73411	AAX87536	AAX87535	AAA38934	AAX87506	AAX87537	AAT09940	AAZ99417
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15.1	15.1	15.1	15.1	15.0	15.0	15.0	14.9	14.9	14.9	14.4	13.9	13.9	13.8	13.8	12.9	12.9	12.9	12.9	12.8	12.2	11.3
9.4	407.2	407.2	407.2	404.4	404.4	404.4	401.8	401.8	401.8	390.6	376.4	375	373.4	372.8	347.8	347.8	347.8	347.8	346.2	329.6	306
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AAA	AAA38937											
e k	AAA38937 standard; DNA; 2861 BP.	вtа	dard;	Ñ.	7	198	BP.					
23	AAA38937;											
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S S	Grand fir abietadiene synthase DNA seguence SEO ID NO:55.	abi	ietadi	ene	SVI	thas	e DN	seque	nce	SEO	E	NO:55

ALIGNMENTS

Synthase; protein co-ordinate data; active site; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antitumour; steroid hormone; signal transduction pathway; bile acid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent; ds. WO200017327-A2 Abies grandis.

(SALK) SALK INST BIOLOGICAL STUDIES KENTUCKY RES DEPT 98US-0100993P. 99US-0130628P. 99US-0150262P. 99WO-US021419 18-SEP-1998; 22-APR-1999; 23-AUG-1999; 17-SEP-1999; (KENT) UNIV 30-MAR-2000

Chappell J, Manna KR, Noel JP, Starks CM; WPI; 2000-292839/25. P-PSDB; AAY90858. Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.

The present invention describes an isolated terpene synthase (1) comprising a region with at least 20% identity to region 265-535 of a 548 Disclosure; Page 439-443; 450pp; English.

carbon atoms (alphac) that have interationic distances, between each other, within tabulated ranges, have a centre point (within a sphere of ardius 2:3 Angstrom) within tabulated ranges, and have an ordered arrangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and collect enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precursors of steroid chormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids encoding them) are used as controls in the analysis of products formed by carymatic synthesis; as nutrient supplements; for affinity purification of isopremoids, or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthases may produce novel terpene products. ApA38910 to AAA38938 and AAY90831 to AAY90859 represent invention AAY90831. (I) contains nine alpha given in sequence (Ia),

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Sequence 2861 BP; 890 A; 514 C; 639 G; 818 T; 0 U; 0 Other;

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1009 AAACGATGCCTCCACTTTCTCAACTTCGTGCTCAGCAAATTTGGCGACTACGTTCCTTGC 1069 aaaagrigcrirggarircrigaacrirgrcrigaagaaarricggaaaccargrigcrirgr 1043 889 829 804 GCTAAGCTTAAAAGGATTCCCACTGATGTTCTCTATGCCCTTCCAACAACAACGTTATTGTAT 863 923 GTGCAGAAAGGGGTTTGAGTTTTGTGAGAAAACACATGGAAGAAATGAAGGACGAAGCTGAC 709 769 803 383 469 443 529 589 563 649 623 TTGGGATTGGATCTTCCTTATCACCTCCCTTTCATCTCCCAAAATCCAAAAAGCGCCAG AAAAAGCTTCAAAAGATTCCCCTCAATGTTCTTCATAACCATCAGACGGCGTTGCTCAC GITITAAACACTCCCGCCTGCCTCCTCACAAATATGGAATAAGGGCGACATTCAA rcittiggaaggititacaagaaatagitagacitggcagaaataataaaacticaatgcaag GACGGATCATTTTAAGCTCCCCTGCATCTACTGCTTGTGTCTTCATGCACACTCAAAAC 564 ahachesenakakhrekandanahahakkekhrakeerichekenakakakakakaka AATCACAGGCCAAGTGGATTCGAGGTCGTGTTTCCTGCAATGTTAGATGAAGCAAAAAGC CAGTCCATGGGCGACGGTGAAACGAATCCATCTGCATATGATACAGCTTGGGTGGCAAGA ATTCCGTCAATTGACGGCTCTGGTGCACCCCAATTTCCCCCAAACGCTTCAATGGATTCTG GTCGATGAGAATCAATAAAAGAATCCAGACATTGGTGAAGGAAATCCAGTGCATGTTT Gaps 15; Length 2861; Score 1091.4; DB 3; Length Pred. No. 1.4e-284; 0; Mismatches 713; Indels AACAATCAACTGCCAGATGGCTCGTGGGGTGAGGAGTGCATTTTT Query Match
Best Local Similarity 68.4%;
Matches 1574; Conservative 830 864 950 924 530 590 650 624 710 684 770 744 890 324 410 384 470 444 350

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rregga craggr	TACTGG CATTGG	GACACT	CTGGAG TTAAAA	GGTGTG GGAGTT	ATAATG ATCATG	AACGCA GATGCC	aagtat aaatat	GGATCA 	aaatat aagtat	ACTCAA CTTCAA	CAGCGG GAGCGT	GCTTGT NAGTGC	GACACC	ratctct rctatca	CAACACA CAATACT	CTATCTT	2090 CGAAAAGTAIGGGAGGGCITGCICGCATĠGTATACCAAAGAAGCCGAATGGICGGCAGCA 214
GAACGC GAGCGG	TATAGG TACAGG	GTCGAT	GATGTT GATGTT	SCAAATT CAGAGA	IGAAAAG GAAACG	AAAAAC AATGTG	GCTATA GCACTC	SCAATTT 	CAACGAA SAATGAA	aaaggag acagag	CACCCGC	ATTCGCT GTTTTCT	rcrrra rcrrra	ATGGGA7 ATGGGA7	GCTGTAC TTTCTAC	GCTGGG GCTAGG	ATGGTC(ATGGTC
racagti racagti	rracgri rrargri	rccrgar rccrgar	ATCTTC: ATCCTC:	rcaaacc rcaaacz	rccggg 	TCTTGC(TCTGGA	GGAGTA: AGAGTA:	CATAGA(TATTGA	TGTGAG	ACACCA.	TACATT GAATTT	GCCAGA 	AGACGA PAGATGA	CCGAAG	ccrage rgreee	STGATGT SCGATGT	AAGCCGA AAGCAGA
TGTCGA: GGTTGA:	TCTGGA: ATTGGA:	rccrar rccrer	CAATGT	recced	ATGTTT TTCATT	AAATGC GAATGC	AGAGGT AGAGGT	AAGTTA	GCTATA 	AGGCCTT 	ATGATCT CGGATCT	rerrrea rcrrrea	rratici 	AAGCGGT AATCAGT	rrrgcri rargrri	AAGGCCC AAGGGCC	CCAAAGI CGAAAGI
CTGGGC GTGGGO	AGAATC IGGAAGC	ATGCAA - SAGAGAA	TGGATA TGGATA	TTTGCTT	SACAAGT	ATCTCCA ATCTGAG	7700790 	AGGCAAG AGGCTAG	ATAAGAT ATATGAT	rggracy Aggracy	GATTCA GTTTCAC	TTAGTA1 CCTTTA1	rcgcagi 	TCTCTG TCACAG	TGAAAG TGAAAA	AGGAACI - AGAGGCI	CGTATA CTTACA
AACGCCI	AAATCAA AGATCAA	aggcaag aggcgac	SACTICA SATIACA	ACTTCT	GATGTTC	CAAATC	AGGATC: AGAATA:	GATTGG GGTTGG	CTGTGT.	TCAATA TCAATA	AATCGG CATCCG	TGGCGG	CTTGCC	AATTGT AGTTGT	ATCAGT	SCACTCA SCACGTG	TCGCAT
TATTTG/ TATTTG/	agaaagi 	TGGGAT	TCCTGA TCTTGA	AAGGAG ATGGGG	TTTATA TCAATO	TCACTA GTACCG	TTAAAA	TGCCAA	GGAAGA GAAAAA	TIGGACT	rggagag rggaaat	TTCTCAG 	AGACTI	SATCTIP SATCTIP	CGGGATA ATGCCAC	AAAGATC	GCTTGC GTCCAAC
TTGATC	ATTTCA 	GAGGCG GAGGCA	TTAGAA TTCGAA	ACGAGA 	TTAACC	AAGACCT	resecto resecti	AGAAGTP AAGAGTP	rggcrgc rggcrrc	GCCAAA1 GCGAAAC	AGCTGG1 AGGTGG1	ATGTATT ATATATT	TATGCC TATACA	CTGGATC TTAGACC	AGCGTT(CCAA	TTTGGA ATAGCA	TGGGAG TGGAAA
racccac ratcccc	SATCGCT SATCGTC	GCGAA? CGAA?	ATGGGTC ATGGGCC	TCAGAC	SATAATO SACATG	GAAGCTZ GAAGCAZ	GATAAG: GACAAA:	TGGCATA TGGCATA	GATGTC GATGTG	GAGCTG	ATTGTC CTTCGA	GTGGAA ACGGAA	ATTGCC GAGGTT	GGATCT	CTGGAT GTGGA-	BAATGGA	AAAGTA AATGTT
CAT	A ATCC	GACC	0 GCC	O AAT	0 ACC	O GAA	o TTT 0 1	0 CCG	O AAT	O TTG	O CAC	10 CCT	O AGA	10 CS CS CS	70 GTC 41 CTP	30 GTC 	90 CGF
107	113	119	125	131	137	143	149	155	161	167	173	179	185	191	197	203	50 50

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1031 AACTICGIGCICAGCAAAITIGGCGACTACGIICCTIGCCATTACCCACTIGAICTAIT 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the sequence of a computer-generated nucleic acid coding for a grand fir (Ables grandis) E-alpha-bisabolene synthase polypeptide (see AAV6557) that has conservative amino acid substitutions relative to the native E-alpha-bisabolene synthase sequence given in AAV66562. E-alpha-bisabolene synthase is a wound- inducible enzyme capable of generating multiple sesquiterpenes, especially E-alpha-bisabolene, from farnesyl diphosphate. The invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing praduction of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenolds, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGTGGACTGGCAAGAGATCACAAATCTTCAATCAAGAGACGGATCATTTTTAAGCTCC 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               718 ATAGITGAAIGGGAACGAAIAAIGGAAGITCAAAGICAGGAIGGGICITICTIAAGCICA 777
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                                                                                                                                                                                                                                                                                                                                                                                      Length 2525;
                                                                                                                                                                                                                                                                                                                                                    Sequence 2525 BP; 749 A; 498 C; 600 G; 678 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                      / Match 27.0%; Score 731.6; DB 2; Local Similarity 59.7%; Pred. No. 3.6e-187; Nes 1369; Conservative 0; Mismatches 894;
 useful for sesquiterpenoid production.
                                      Example 11; Page 95-98; 136pp; English.
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Matches 1369;
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                     GATATITACAAAAGACIGGITITIGAAACIGCAAGAATAAIGCAACICTITIAIAIGCAA 2531
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gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour; ss.
 AAGTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCG
                                                                                                                                                                        AAAATTGATCGCGAATCTAGATTTCTTCAACTCATGGGCTTAACAGGCGCTTTGGTGAAT
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                                                                          ACAGTCGTACTAAACTCAATCTTTTTCACTGGAGAATTACTTCCTGATTACATTTTACAG
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                                                                                                                                               CAAGTAGACCTTCGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTAATCAAT
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                                                                                                                                                                                                                                                                                                                                 TATATGAAGGACCATCCTAAAATCTCTGAAGAAGAAGCTCTACAACATGTCTATAGTGTC
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P-PSDB; AAY06567.
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                                                                                                                                                                                                                                          AATCCGGAGTGCACAGAGGAAGAAGCTCTAAGTCATGTTATGGTATCATCGACAACGCA 2461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycrene synthase; limonene synthase; pinene synthase; flavour;
monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGATGCTTTTCGAGGAGACAAGAGTGACGATGGTGATATTCAAGGATGGAGATGGATTC
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P-PSDB; AAW85703.
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fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene.

Example 1; Page 86-90; 121pp; English

The state of the s Nucleotide sequences encoding mycrene synthase, limonene synthase and ##*##

Sequence 2424 BP; 730 A; 472 C; 575 G; 647 T; 0 U; 0 Other;

613 673 GAGGTCGTGTTTCCTGCAATGTTAGATGAAGCAAAAAGCTTGGGATTGGATCTTCCTTAT 790 CACCTCCCTTTCATCTCCCAAATCCACCAAAAGCGCCAGAAAAAAGCTTCAAAAGATTCCC 850 CTCAATGTTCTTCATAACCATCAGACGGCGTTGCTCTACTCTCTGGAGGGTTTGCAAGAT 910 GTGGTGGACTGGCAAGAGATCACAAATCTTCAATCAAGAGGACGGATCATTTTTAAGCTCC 970 CGCCCGCAATTTCCCCAAACAGTTGACTGGATTTTGAAAAACCAGTTAAAAGATGGTTCA 253 circrecricaranegaacerregearcrecaagragaegeageaarreaaran 373 AGAAAACACATGGAAGAATGAAGGACGAAGCTGACAATCACAG---GCCAAGTGGATTC 730 AAGAGCAATCTGGAACTAGTAAAGGATGAAACCGATCAAGATAGCTTGGTAACAGACTTT 433 GAGATCATATTTCCTTCTCTGTTAAGAGAAGCTCAATCTCTGCGCCTCGGACTTCCCTAC 493 GACCIGCCITATATACATCITGCAGACIAAACGGCAGGAAAGATTAGCAAAACTTTCA 553 AGGGAGGAAATTTATGCGGTTCCGTCGCCATTGTTGTATTCTTTAGAGGGAATACAAGAT GCACCCCAATTTCCCCAAACGCTTCAATGGATTCTGAACAATCAACTGCCAGATGGCTCG CTCACTCTCAAAATATGGAATAAGGGCGACATTCAAGTGCAGAAAGGGGTTGAGTTTGTG Acrocarcrectrareacacagearegrasceaegegegegegerarrearegererecr AATCCATCTGCATATGATACAGCTTGGGTGGCAAGAATTCCGTCAATTGACGGCTCTGGT Gaps 34; Score 730.2; DB 2; Length 2424; Pred. No. 8.5e-187; 0; Mismatches 893; Indels 34; Query Match 27.0%; Best Local Similarity 59.6%; Matches 1370; Conservative 434 194 791 134 494 254 314 674 374 434 494 851 554 971 554 731 ठ व ठ g 8 8 6 8 6 셤 ò 음 참 ઠ Š જે 음 중 음

1450 1150 1810 1270 ACTAAATATTTGAGAGAAGCTCTTGAGAAAAGTGAGACTTCCAGTGCATGGAACAACAAA 1210 1631 ACTGTGTATAAGATGCTATATGTGAGCAAQAAATATTTGGAGCTGGCCAAATTGGAC 1690 GAAATCAAAGAATCTCTGGATTACGTTTATAGGTACTGGGACGCCGAAAGAGGCGTGGGA 1210 971 cecrecaraceracarerarereceaecearrirraacaacricaaagareceaareee 1030 ACABATCATCTCCAAAATGCTCTTGCCAAAAACAACGCATTTGATAAGTGGGCTGTCAAG 1510 1511 AAGGATCTTCCTGGAGGGGGGAGTATGCTATAAAGTATCCGTGGCATAGAAGTATGCCA 1570 CAAAACCTGAGCCAAGAGATCAAATACGCGCTGAAGACTTCTTGGCATGCCAGTGTTCCG 1270 agagricgaagcaaagagaractgagagagrgrarcgcccagarrargcacgcaragcaaaa 1330 1331 TGCGTTTACAAGCTACCCTACGTGAACAATGAAAGTTTTTAGAGCTGGGAAAATTAGAT 1390 rrchacarrarccaccarccaccaagaagaaraargaagaargrraccagcrocrrada 1450 GATTCGCGGTTGCCACTATTCACCTTCGCTCGGGAGGCCGCTGGAATTCTACTTA 1510 GTGGCGGTTAGTATGTTTGAGCCAGAATTCGCTGCTTGTAGAATTGCCTATGCCAAGACT 1870 Graccececesarcerarida accesara receasara e de contra cana de contra contra contra de c 1571 GCATGCTTGCAGACTGTTCTGGACGATATGTATGACACTTATGGAACCCTAGATGAATTG 1630 AAATTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTGGATAGCGTTCGGGAT 1990 1991 AATCAGTTGAAAGTTTGCTTCCTAGGGCTGTACAACACAGTGAATGGATTTGGAAAAGAT 2050 GGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAAAAGTATGGGAGGGCTTG 2110 GCAGAGAAACAGGGGCGTGAATTGGTCACTTTTTCAGAAAGGATGGGAGGATTAT 1807 AACTICGIGCICAGCAAATTIGGCGACTACGTICCITGCCATTACCCACTIGATCTATTT 1090 1271 AGACTTCATGGATACAATGTATCTTCAGATGTTCTGGAGAATTTTCAGAGACGAGAAAGGA 1330 TAT---ATGAAACTATGTTACCAAATCTATTATGACATAGTTCACGAGGTGGCTTGGGAG 1747 854 GAAATCAAGGAAGCTCTTGATTATGTTTACAGGCATTGGAACG---AAAGAGGAATTGGG 910 794 GAACGCCTGTTGATCGTAGATAATATTGTACGCCTTGGAATCTATAGACACTTTGAAAAG 853 911 TGGGGCAGACTAAATCCCATAGCAGATCTTGAGACCACTGCTTTGGGATTTCGATTGCTT 970 TGGGCAAGATGCAATCCTAATTCCTGATGTCGATGACACTGCCATGGGTCTTAGAATCCTG TCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACACCCACGGATCTCTGGATGATCTT AGATGTTCACAAGTATGTTTTCCGGGAGAAAAGATAATGGAAGAAGAAGCTAAGACCTTCACT <u> adalectrice de contrace de adada a carretra a adecra a a contra a a a contra a a a contra a a a contra a a contra a a contra a contra a a contra a a contra a a contra a con</u> TTCAATATGGTGCAGGCCTTACACCAAAAGGAGACTCAACACATTGTCAGCTGGTGGAGA CCTGCTTCTACTGCCTGCGTTTTCATGCACACAGAGACGCGAAATGCCTTGAATTCTTG GACTICITITGCITITGCCGGTCAAACGCAAAITGGTGTGACCGAIAAICITAACCTITAI GAATCGGGATTCAATGATCTTACATTCACCGGCCAGCGGCCTGTGGAAATGTATTTCTCA 1631 1031 1091 1151 1211 1331 1391 1001 1451 1151 1571 1271 1691 1391 1751 1451 1811 1511 1871 1931 2051 1748 유 g g g 용 쉱 à 용 કે 용 ò 셤 ઠે 셤 à 셤 è 셤 Š 셤 ò 음 જે 셤 ઠે 셤 8 셤 ò 셤 8 ठे ò ठे ઠે 8

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                         TTTTTCA---CTGGAGAATTACTTCCTGATTACATTTTACAGCAAGTAGACCTTCGGTCC 2287
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             CICGCATCGIATACCAAAGAAGCCGAATGGICGGCAGCAAAGIATGTGCCGACATTCAAC 2170
                                                                                1868 GAGTACATAAAGAATGGAATCACATCTATCGGCCAACGTATACTTCTGTTGAGTGGAGTG 1927
                                                                                                                          trgataataggatigggcaacticchtrcgcaagaggcattagagaaagtagattatccagga
                                                                                                                                                                  AGACGTGTTCTCACAGAGCTGAATAGCCTCATTTCCCGCCTGGCGGATGACACGAAGACA
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RESULT

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17-SEP-1999; 18-SEP-1998;

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The present invention describes an isolated terpene synthase (I)

Comprising a region with at least 20% identity to region 265-535 of a 548

comprising a region with at least 20% identity to region 265-535 of a mino acid (as) sequence (la), given in hAX908131. (I) contains nine alpha carbon atoms (alphaC) that have interactomic distances, between each other, within tabulated ranges, and have an ordered aranges, and have an ordered arrangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and cralted arrangements (tables given in the specification). (I), and crelated enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precursors of steering confidences and bile acids, as photoreceptors and as co-factor side chains. Components of signal transduction pathways, precursors of steering by encoding them) are used as controls in the analysis of products formed by encoding them) are used as controls in the analysis of products formed by controling expression of terpene synthases or inheritance of the gene in plant breeding programs. The new synthases may produce novel terpene cycloproducts. AAA38910 to AAA38938 and AAY90831 to AAX90859 represent invention
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                                                                                                                                                                                                                                                                                                                                                    Novel terpene synthase enzymes, ussful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
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59.6%; Pred. No. 8.5e-187;
tive 0; Mismatches 893;
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                                                                                                                                                                                               Starks
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INST BIOLOGICAL STUDIES.
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Matches 1370; Conservative
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                                                                                                                                                                                                                              New nucleic acid encoding monoterpene synthases, for increasing synthesis in plants, e.g. for increasing resistance to pests or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 730.2; DB 4; Length 2424;
Pred. No. 8.5e-187;
0; Mismatches 893; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2424 BP; 730 A; 472 C; 575 G; 647 T; 0 U; 0 Other;
                                                                                                                                                      Phillips MA
                                                                                                                                                                                                                                                                                                     Example 1; Page 119-122; 175pp; English
                                                                                                                        FOUND
                                                                                                                                                        Croteu RB,
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                                                                                                                        (UNIW ) UNIV WASHINGTON STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match 27.0%;
st Local Similarity 59.6%;
tches 1370; Conservative
                                                                                         99US-00360545
                                                           24-JUL-2000; 2000WO-US020264
                                                                                                                                                        Bohlmann J,
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P-PSDB; AAB69373.
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Steele CL;

Bohlman J, Jetter R,

Crock JE,

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                                                              WPI; 1999-458569/38.
P-PSDB; AAY06566.
        22-JAN-1998;
                                             Croteau RB,
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                   TIGATAATGGATGGGCAACTCCTTTTGGAAGAGGCATTAGAGAAAGTAGATTATCCAGGA
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                                           GAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCAATC
                                                             GAGTACATAAAGAATGGAATCACATCTATCGGCCAACGTATACTTCTGTTGAGTGGAGTG
                                                                               TITITCA----CIGGAGAATTACTTCCIGATTACATTTTACAGCAAGTAGACCTTCGGTCC
                                                                                                                   AAATTTCTGC-----ATCTTGTGTCTTTGACTGGACTAATCAATGACACCAAGACT
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                                                                                                                                                                       TATAAAGCTGAGAAGCGTCGAGAATTGGCGTCCAGCATTGAATGTTACATGAAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .2454
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fir B-alpha-bisabolene synthase cDNA
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99WO-US001300

21-JAN-1999;

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This is the nucleotide sequence of grand fir (Abies grandis) B-alphabisabolene-synthase CDNA. It codes for a wound-inducible enzyme (see AAY06566) that is capable of generating multiple sesquiterpenes. especially B-alpha-bisabolene, from farnesyl diphosphate. The full-length CDNA was obtained by 5'RACE from a wound-induced grand fir stem CDNA library. It differs from the sequence of clone AG1, provided in AAX87504, by a single nucleotide at position 194 (C is AG1, T in the present sequence) that results in an amino acid change from Ala-65 in AG1 to Vale5 in the protein of AAY06566. The present sequence is believed to be the correct sequence of grand fir B-alpha-bisabolene synthase CDNA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           730
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Grand fir (Abies grandis) sesquiterpene synthase genes and products, useful for sesquiterpenoid production.
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Pred. No. 8.6e-187;
0; Mismatches 893;
                                                                                                            Example 11; Page 89-92; 136pp; English
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llarity 59.6%;
Conservative
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Best Local Similarity
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gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour; ss.
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                                          8
                                                                                                                                                                                                                                                                                                                                                                                                 This is the sequence of a computer-generated nucleic acid coding for a grand fir (Abies grandis) E-alpha-bisabolene synthase polypeptide (see AXV06568) that has conservative amino acid substitutions relative to the native E-alpha-bisabolene synthase sequence given in AAV06562. E-alpha-bisabolene synthase is a wound- inducible enzyme capable of generating multiple sesquiterpenes, especially E-alpha-bisabolene, from farnesyl capholate. The invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, sesquiterpene synthase in a prokaryotic or eukaryotic production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives
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                                                                                                                                                                                                                                                                                           Grand fir (Abies grandis) sesquiterpene synthase genes and protein products, useful for sesquiterpenoid production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
27.0%; Score 730.2; DB 2; Length 2528;
Best Local Similarity 59.6%; Pred. No. 8.6e-187;
Matches 1370; Conservative 0; Mismatches 893; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2528 BP; 750 A; 498 C; 599 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                               ij
                                                                                                                                                                               Steele
                                                                                                                                                                               Jetter R,
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                                                                                                                                    FOUND.
                                                                                                                                                                               Bohlman J,
                                                                                                                               (UNIW ) UNIV WASHINGTON STATE RES
                                            99WO-US001300
                                                                                       98US-0072204P
                                                                                                                                                                               Crock JE,
                                                                                                                                                                                                                         WPI; 1999-458569/38.
P-PSDB; AAY06568.
                                          21-JAN-1999;
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products, useful for sesquiterpenoid production.
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                                                                                                                    WPI; 1999-458569/38.
                                                                                                                               P-PSDB; AAY06562.
                              21-JAN-1999;
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                               E-alpha-bisabolene synthase; grand fir; sesquiterpene synthase; gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour; ss.
                                                                                               2171 GAATATGTGGAAAATGCCGAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCAATC
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/note= "C in clone of AAX87529"
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This is the nucleotide sequence of the grand fir (Abies grandis) E-alphablaabolene synthase full-length cDNA insert of plasmid pAG1. The CDNA clone codes for a 817-amino acid wound-inducible enzyme (see AAXV6562) that is capable of generating multiple sesquiterpenes, especially E-alphabla constant from farnesyl diphosphate. The full-length cDNA was obtained by 5'RACE from a wound-induced grand fir stem cDNA library. A separately consolution (see AAX87529) contains a single nucleotide difference from AG1 (T for C at position 238) and is believed to be the correct sequence for grand fir E-bisabolene synthase. The invention provides of granosperm sequiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or enkaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter cellogical interactions mediated by farnesyl diphosphate and its
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Pred. No. 8.7e-187;
0; Mismatches 893;
Claim 9; Page 68-71; 136pp; English.
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                                                                                                                                                  AACTICGIGCICAGCAAAITIGGCGACTACGIIICCIIIGCCAIIACCCACTIGAICIAITI 1090
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                                                                                                                                                                                                                                                                                                      762 ATAGTTGAATGGGAACGAATAATGGAAGTTCAAAGTCAGGATGGGTCTTTTAAGCTCA 821
AGGGAGGAAATTTATGCGGTTCCGTCGCCATTGTTGTATTCTTTAGAGGGAATACAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a pacific yew taxadiene synthase (TS). The sequence can be used to increase taxol blosynthesis into taxoids in transformed ceals. The nucleic acid sequences can be modified to produce proteins with improved efficiency, and to redirect the targeting of the expressed polypeptide. The modifications can be to alter catalytic efficiency, to modify substrate utilisation, and to alter product outcome. The antibodies specific for the mature native pacific yew TS polypeptide can be used to purify TS polypeptides, cloning TS homologues from Pacific yew or other plant species, and as probes for blots and immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676
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Pred. No. 6.1e-163;
0; Mismatches 913; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2700 BP; 819 A; 541 C; 616 G; 724 T; 0 U; 0 Other;
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Best Local Similarity 57.7%;
Matches 1302; Conservative
                                                                                                                                                                                                               97WO-US006320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthase; protein co-ordinate data; active site; modification; terpenoid;
                                                                                      2081 GTTATGTACAAGAAAGGGAGTGGCTTGAAGCCGGGTATATACCAACTTTTGAAGAGTACT
                                                                                                                                                                                                                2261 AGCTTGTATCCTTGAGCTGGCGACTAACAAACGACAAAACAAAACAAAAAAAGG
                                                                                                                                                                                                                                                         TARAGACTTATGCTATATCAGTAGGCCTTGGACCGTGTACCTACAACAATACTACTAA
                                                                                                                                                         2238 CTGGAGAATTACTTCCTGATTACATTTTACAGCAAGTAGACCTTCGGTCCAAATTTCTGC
                                                                                                                                                                              2201 TGGGTGAGCTTGTGAAAGATGATGTTGTTGAGAAAGTGCACTATCCCTCAAATATGTTTG
                                                                                                                                                                                                   2298 ATCTTGTGTCTTTGACTGGACGACTAATCAATGACACCAAGACTTACCAGGCCGAGAAA
                                                                                                                                                                                                                                            2358 ACCGTGGTGATTGGTTTCCAGCGTACAGTGCTACATGAGGGAAAATCCGGAGTGCACAG
                                                                                                                                                                                                                                                                                      AGGAAGAAGCTCTAAGTCATGTTTATGGTATCATCGACAACGCACTGAAGGAATTGAATT
                                                                                                                                                                                                                                                                                                                             2441 TTGAATATTTCAAACCATCCAATGATATCCCAATGGGTTGCAAGTCCTTTATTTTTAACC
                                                                                                                                                                                                                                                                                                                                                                       CTGCAAGAGTGATGCAGCTGTTTTATATGTACAGAGATGGCTTTGGTATCTCTGACAAAG
                                                   <u>accracaccaccarcarcarcarcarcaraacaaaaacccroccacarraracrarrara</u>
                                                                        2118 CGTATACCAAAGAAGCCGAATGGTCGGCAGCAAAGTATGTGCCGACATTCAACGAATATG
                                                                                                                TGGAAAATGCCAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCAATCTTTTCA
                                                                                                                                                                                                                                                                                                        3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antitumour; steroid hormone; signal transduction pathway; bile acid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent; ds.
                                AGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAAAAGTATGGGAGGCCTTGCTCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATTAAGGACTATATAAGAAAAGTTTATATTGATCC 2597
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                                                                                                                                                                                                                                                                                                                                                                                                               AGATGAAAGACCATGTCAGCCGAACTCTTTTCGATCC
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22-APR-1999;
23-AUG-1999;
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comprising a region with at least 20% identity to region 255-535 of a 548 mino acid (aa) sequence (la), given in AAY90831. (I) contains nine alpha carbon actoms (alphaC) that have interatomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom) within tabulated ranges, and have an ordered rangement of R groups (defining as side chalms), excluding specific tabulated arrangement of R groups (defining as side chalms), excluding specific tabulated arrangements (tables given in the specification). (I), and related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precursors of steroid components of signal transduction pathways, precursors of steroid components of signal transduction pathways, precursors of steroid conding them) are used as controls in the analysis of products formed by enzymatic synthesis; as nutrient supplements; for affinity purification of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthases may produce novel terpene products. AAA38910 to AAA3893 and AAY90851 to AAA38910 to AAA3893 and AAY90851 to AAA38910 to geougenessent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                               Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443
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Pred. No. 6.1e-163;
0; Mismatches 913;
                                                                                                                 Noel JP, Starks CM;
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KENTUCKY RES DEPT.
INST BIOLOGICAL STUDIES.
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Best Local Similarity 57.7%;
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                                                                                                                                                                                                                  monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-limonene((-)-alpha-pinene synthase, limonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        963 AAATTGGAGTTCAACATCTTCACTCCCTTCAACAGAAGGAGTTACAGTATCTCTCCAG
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Best Local Similarity 57.6%;
Matches 899; Conservative
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synthesis in plants, e.g.
treatment of cancer.
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Pred. No. 9.3e-102;
0; Mismatches 620; Indels
              insect resistance; nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phillips
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Croteu RB,
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Local Similarity 57.3%;
hes 899; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bohlmann J,
                     terpinolene synthase;
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P-PSDB; AAB69393.
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                                                                                       Abies grandis
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                                                                                                                                                                                                                                                      AAGTATGCCAAGATTGGAGGCAAGAAGTTACATAGAGCAATTTG---GATCAAATGATGT
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                      TAGAATCCTGAGACTTCATGGATACAATGTATCTTCAGATGTTCTGGAGAATTTCAGAGA
                                                                                                                    1321 CGAGAAAGGAGACTTCTTTTGCTGTTTGCTCAAACGCAAATTGGTGTGACCGATAATCT
                                                                                                                                                                rcaaaareeacagrirgrarecreceeercagacagagagagagaagagageerrer
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                                                                                                                                                                                                                                                                                                              Mycrene synthase, limonene synthase, pinene synthase, flavour, monoterpene synthase, aroma, defense, plant seed, oil, meal, primer, PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequences encoding mycrene synthase, limonene synthase and pinene synthase from Grand fir may be incorporated into any organism (e.g. intect plant, animal, microbe), or derived cell culture that produces geranyl diphosphate for the production of the aforementioned enzymes or their products. The sequences when expressed in transfected cells may also be used for the production or modification of flavour and aroma properties, improvement of defense capability, and the alteration of other ecological interactions mediated by mycrene, limonene, pinene, or their derivatives. In particular they can be used for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                   Grand Fir monoterpene synthase clone AG3.48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoterpene synthases, for increasing terpene for increasing resistance to pests or for
                    CTGCTACAAGGCCGATAGGGATCGTGTGAAGAAGCTTCGTGTATATCATGTTATAAA
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      GACTTACCAGGCCGAGAGAAACCGTGGTGAATTGGTTTCCAGCGTACAGTGCTACATGAG
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                                             GGAAAATCCGGAGTGCACACAGAAGAAGCTCTAAGTCATGTTTATGGTATCATCGACAA
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                                                                                                                                                                                                                                                                                                                                                           Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; myrcene synthase; (-)-limonene synthase; terpinolene synthase; insect resistance; nutrition; ss.
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                                                                          GCCAACGTTTGAAGAGTACCATGAGAATGGGAAAGTGAGCTCTGCATATCGCGTAGCAAC 1510
                                                                                                                                    ATTGCAACCCATCCTCACTTTGAATGCATGCCTTCCTGATTACATCTTGAAGGGAATTGA 1570
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                                                                                                       ACTAAACTCAATCTTTTTCACTGGAGAATTACTTCCTGATTACATTTACAGCAAGTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grand fir delta-selinene synthase DNA sequence SEQ ID NO:47.
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The present invention describes an isolated terpene synthase (1)

Comprising a region with at least 20% identity to region 265-535 of a 548

amino acid (aa) sequence (1a), given in AAY90831. (1) contains nine alpha
carbon atoms (alphaC) that have interactomic distances, between each
carbon atoms (alphaC) that have interactomic distances, between each
cother, within tabulated ranges, have a centre point (within a sphere of
radius 2.3 Angstrom ) within tabulated aranges, and have an ordered
arrangement of R groups (defining as side chains), excluding specific
carbulated arrangements (tables given in the specification). (1), and
related arrangements (tables given in the specification). (1), and
related enzymes, are used to produce a wide range of terpenoids (e.g.
cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances,
flavours, pheromones, defensive agents, pigments, antitumour agents,
components of signal transduction pathways, precursors of steroid
bormones and bile acids, as photoreceptors and as co-factor side chains.
Some synthases with little or no catalytic activity (and nucleic acids
correcting expression of terpene synthases or inheritence of the gene in
collispicating expression of terpene synthases may produce novel terpene
contonering programs. The new synthases may produce novel terpene
products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAGAGGCGTGGGATGGGAAGATGCAATCCTATTCCTGATGTCGATGACACTGCCATG 1255
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                                                                                                      Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardarrraarcaaacercrrcagarcerreacacrrragaareccreegaarcearaga 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences used in the exemplification of the present invention
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57.4%; Pred. No. 1.8e-100;
tive 0; Mismatches 623;
Starks CM;
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Noel JP,
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Manna KR,
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Matches 903; Conserv
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Chappell J,
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                                                                                                                                                                                                                                                                                                                                                                                                GCTTGTAGAATTGCCTATGCCAAGACTTCTTGCCTCGCAGTTATTCTAGACGATCTTTAC 1903
                                                                                                                                                                                                                                                                                                                                                                                                                            GGATCAAATGATGTCTGGCTGGGGAAGACTGTGTATAAGATGCTATATGTGAGCAACGAA 1663
                                                                                                                               AAATATTTGGAGCTGGCCAAATTGGACTTCAATATGGTGCAGGCCTTACACCAAAAGGAG 1723
                                                                                                                                                                                                                     ACTCAACACATTGTCAGGTGGTGGAGAATCGGGATTCAATGATCTTACATTCACCCGC 1783
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                                                                                        -----CAACCAA 762
GAGITITCCAIGGCAITGCCAGAGGCGAGAGGCAAGGAGCTITCTCGAAATAIAI 723
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                                                                                                                                                                                                                                                                 823 ATACAGTTTATTACAAGGTGGTGGAGAGACTCGGGTATATCGCAGCTGAATTTCTATCGA
                                                                                                                                                                                                                                                                                                             CAGCGGCCTGTGGAAATGTATTTCTCAGTGGCGGTTAGTATGTTTTGAGCCAGAATTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1063 CITICGTIGACAGAIGACCICCCAGAC---TACAITAAATIGCATICCAGTICTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u> AATACAGTGAATTGAATTGAAATCGTGAAACGGCAAGGGCGGGATATGACAACC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2084 TATCTTCGAAAAGTATGGGAGGCTTGCTCGCATCGTATACCAAAGAAGCCGAATGGTCG
                                                                                                                                                           AACACAGTGAATGGATTTGGAAAAGATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGC
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                                                                                                                                                                                                                                               Search time 181.026 Seconds (without alignments) 8292.408 Million cell updates/sec
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/cgn2_6/ptodata2/ina/6A_COMB.seq:*
/cgn2_6/ptodata2/ina/PCTUS_COMB.seq:*
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US-09-234-393-39
US-09-234-393-1
US-09-365-171-1
US-09-365-171-1
US-09-398-395A-45
US-09-398-395A-45
US-09-398-395A-45
US-09-398-395A-45
US-09-303-0128-45
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US-09-303-0128-45
US-09-303-0128-45
US-09-234-393-37
US-09-234-393-37
US-09-234-393-11
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US-09-360-545-66
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US-09-380-358-47
US-09-897-586A-47
US-09-903-012B-47
US-09-903-0797-47
US-09-234-393-43
US-09-234-393-45
US-09-2865-171-45
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Fatent No. 646872
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Rathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395A
CURRENT APPLICATION NUMBER: 60/100,993
FRIOR APPLICATION NUMBER: 60/100,993
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR PILING DATE: 1999-04-22
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FREESEQ for Windows Version 3.0
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Pred. No. 0;
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                                  AAACGATGCCTCCACTTTCTCAACTTCGTGCTCAGCAAATTTGGCGACTACGTTCCTTGC
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       APPLICANT: Chappell, Joseph
APPLICANT: No. 64953541, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT PAPLICATION NUMBER: US/09/887,586A
CURRENT PILING DATE: 2001-06-22
FRIOR APPLICATION NUMBER: 09/398,395
FRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
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68.4%; Pred. No. 0;
tive 0; Mismatches
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; OTHER INFORMATION: abietadiene synthase US-09-887-586A-55
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Matches 1574; Conservative
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SENERAL INFORMATION:
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GENERAL INFOGRATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 6559291, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: STARKS, COURTNEY M.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT FILING DATE: 2001-06-29
PRIOR PELLING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FRAESEQ for Windows Version 3.0
SED ID NO 55
LENGTH: 2861
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ORGANISM: Ables grandis
PEATURE:
LOCATION: (3)...(2606)
OTHER INFORMATION: abietadiene synthase
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Patent No. 6559297
GENERAL INFORMATION:
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Length 2861
  Score 1091.4; DB 4; Length
Pred. No. 0;
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      40.3%;
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                                                                                                                                                                                                                                                                                                                                              Sequence 55, Application US/09903012B
Patent No. 6569656
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REPRENCE: 07678-02501,
CURRENT PAPLICATION NUMBER: US/09/903,012B
CURRENT PELING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
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OTHER INFORMATION: abietadiene synthase
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ORGANISM: Abies grandis
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Pred. No. 0;
0; Mismatches
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/900,797
CURRENT FILING DATE: 2001-07-06
FRIOR APPLICATION NUMBER: US/09/398,395
FRIOR PILING DATE: 1999-09-17
FRIOR PILING DATE: 1999-04-22
FRIOR PILING DATE: 1999-04-22
FRIOR PILING DATE: 1999-04-22
FRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTESQ FOR WINDOWS VERSION 3.0
SEQ ID NO 55-
LENGTH: 2861
                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
US-09-900-797-55
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ilarity 68.4%;
Conservative
                                                                                                                                                                TYPE: DNA
ORGANISM: Abies grandis
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y Squence 39, Application US/09234393A

y Patent No. 6265639

general INFORMATION:

y APPLICANT: Crock, John E

APPLICANT: Bohlman, Jorg

APPLICANT: Bohlman, Jorg

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: WSUR113345

CURRENT APPLICATION NUMBER: US/09/234,393A

CURRENT APPLICATION NUMBER: US/09/234,393A

KRAITER APPLICATION NUMBER: US/09/224

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 39

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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: E-alpha-bisabolene synthase
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Pred. No. 3.2e-210;
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Best Local Similarity 59.7%;
Matches 1369; Conservative (
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ORGANISM: Artificial Sequence
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US-09-234-393-39
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APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John B
APPLICANT: Crock, John B
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR117468
CURRENT PAPLICATION NUMBER: 05/234,393
FRIOR PILING DATE: 1999-01-20
FRIOR FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PACENTIN VET: 2.00
SEQ ID NO 39
LENGTH. 2525
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Pred. No. 3.2e-210;
0; Mismatches 894;
                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/09865171 Parent No. 6451576 GENERAL INFORMATION:
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US-09-865-171-39
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Patent No. 6265639

GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Norg
APPLICANT: Croteau, Norg
APPLICANT: Bollman, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WGWIL13345

CURRENT APPLICATION NUMBER: US/09/234,393A

CURRENT FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: 60/072,204
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                                                                                    Gaps
                                                                                    34;
                                                                     Length 2424;
                                                                                    Indela
                                                                    Score 730.2; DB 3;
Pred. No. 8.2e-210;
0; Mismatches 893;
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2424
                                                                    Query Match 27.0%;
Best Local Similarity 59.6%;
Matches 1370; Conservative
                                      ; TYPE: DNA
; ORGANISM: Abies grandis
US-09-234-393-1
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971 GGCTGCATAGGTACAATGTATCTCCAGCCATTTTTGACAACTTCAAAGATGCCAATGGG
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| Sequence | 15, Application US/09360545 |
| Patent No. 6429014 |
| GENERAL INFORMATION: |
| APPLICANT: Croteau. Rodney B |
| APPLICANT: Steele, Christopher L |
| APPLICANT: Steele, Christopher L |
| APPLICANT: Steele, Christopher L |
| APPLICANT: William, MonoTenens Synthases FROM GRAND FIR (ABIES GRANDIS) |
| TILE REFERENCE: Weuri3085 |
| CURRENT APPLICATION NUMBER: US/09/360,545 |
| CURRENT FILING DATE: 1999-07-26 |
| EARLIER FILING DATE: 1999-07-26 |
| EARLIER FILING DATE: 1998-07-10 |
| NUMBER OF SEQ ID NOS: 107 |
| SEQ ID NO 15 |
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; OTHER INFORMATION: Clone AG1.28
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Best Local Similarity 59.6
Matches 1370; Conservative
    Croteau, Rodney
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ORGANISM: Abies grandis
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Sequence 1, Application US/09865171 Patent No. 6451576 GENERAL INFORMATION:

1031 AACTICGIGCICAGCAAAITIGGCGACIACGIICCIIGCCAIIACCCACIIGAICIAIII 1090 493 850 910 613 970 673 733 193 553 253 613 313 673 CTTGTGCTCCTTAAATGGAACGTTGGGAATCTGCAAGTAGAGCAGGGAATTGAATTCATA 373 AGAAAACACATGGAAGAAATGAAGGACGAAGCTGACAATCACAG---GCCAAGTGGATTC 730 GAGATCATATTTCCTTCTCTGTTAAGAGAAGCTCAATCTCTGGGCCTCGGACTTCCCTAC 493 553 AACAGTGTGATGATCAAGTTTGGAAATTTTGTTCCCTGCTGTATCCTGTGGATCTGCTG 793 GAACGCCTGTTGATCGTAGATAATATTGTACGCCTTGGAATCTATAGACACTTTGAAAAG 853 GAGGICGIGITICCIGCAATGITAGAIGAAGCAAAAAGCITGGGAITGGAICTICCITAI 790 GRANDIS) 194 CGCCCCCCAATTTCCCCCAAACAGTTGACTGGATTTTGAAAAACCAGTTAAAAGATGGTTCA 614 ATAGTTGAATGGGAACGAATGAATGGAAGTCAAAGTCAGGATGGGTCTTTTCTTAAGCTCA CCTGCTTCTACTGCGCTTTTCATGCACACAGGAGACGCGAAATGCCTTGAATTCTTG 134 ACTCCATCTGCTTATGACACAGCATAGCGAGGGTGCCCGCCATTGATGGCTCTGCT resesaarreacrerrrersersiceaceacererreceaceacrerrerrerrerr CTCACTCTCAAAATATGGAATAAGGGCGACATTCAAGTGCAGAAAGGGGTTGAGTTTGTG CACCTCCCTTTCATCTCCCAAATCCACCAAAAGCGCCAGAAAAAGCTTCAAAAAGATTCCC 554 AGGGAGGAAATTTATGCGGTTCCGTCGCCATTGTTGTATTCTTTAGAGGGAATACAAGAT GTGGTGGACTGGCAAGAGATCACAAATCTTCAATCAAGAGACGGATCATTTTTAAGCTCC GCACCCCAATTTCCCCCAAACGCTTCAATGGATTCTGAACAATCAACTGCCAGATGGCTCG 851 CTCAATGTTCTTCATAACCATCAGACGGCGTTGCTCTTACTCTTGCAGGGTTTGCAAGAT 434 AATCCATCTGCATATGATACAGCTTGGGTGGCAAGAATTCCGTCAATTGACGGCTCTGGT Gaps (ABIES APPLICANT: BOLDA, JOID
APPLICANT: Steele, Christopher L
TITLE OP INVENTION: SEQUITERPENE SYNTHASES FROM GRAND FIR (AB);
TITLE OP INVENTION: SEQUITERPENE SYNTHASES FROM GRAND FIR (AB);
TITLE OF INVENTION: AND METHODS OF USE
FILE REPRENCE: WSUR117468
; CURRENT APPLICATION NUMBER: US/09/865,171
CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/234,393
; PRIOR APPLICATION NUMBER: 09/072,204
PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PATENTIN VOICE: 2.0
; SEQ ID NO 1 Length Indels Score 730.2; DB 4; Pred. No. 8.2e-210; 0; Mismatches 893; 794 용 8 셤

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27.0%; Score 730.2; DB 4; Length 2424;
Best Local Similarity 59.6%; Pred. No. 8.2e-210;
Matches 1370; Conservative 0; Mismatches 893; Indels 34;
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; OTHER INFORMATION: E-alpha-bisabolene synthase US-09-398-395A-45
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ORGANISM: Abies grandis
FEATURE:
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\$54 AGGAGGANATTRATCGGTTCCGCCGCCATTGTTCTATATCTTTAGAGGGAATACATCTT \$11 GTGGTGGATCGCCAGGAGGATCCGTCCAATACAGAGGGAATACATCCTC \$12 CTGGTGATCGTGCCAAGAGGAATATCGAACACAAAAAAAA	1871 TCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACACCCACGGATCTTCGGATGATCTT 1930 1571 GCATGCTTGCAGACTTCTGGACGATATGTATGACACCTTATGGAACCTTAGGAACCTTATGGAACCTTAGGAACTTGTATGAACCCTAGATGATGTATGT
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Decision Control Decision Decision	Db 434 GAGATCATATTTCTTTAGAGAAGCTCAATCTCTGGGCCTCGGACTTCCCTAC 493 Qy 791 CACCTCCCTTTCATCTCCCCAAATCCACCAAAAGCGCCAGAAAAAGCTTCAAAAAGATTCCC 850

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Pred. No. 8.2e-210;
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"LOCATION: (2)...(2347)

COTHER INFORMATION: B-alpha-bisabolene synthase
US-09-895-752-45
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 45
LENGTH: 2424
                                                                                                                                                                                                                                                                                                                                                        Query Match 27.0%;
Best Local Similarity 59.6%;
Matches 1370; Conservative
                                                                                                                                                                   TYPE: DNA ORGANISM: Abies grandis
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APPLICANT: No. 65592971, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REPERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-18
PRIOR PELING DATE: 1998-09-18
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Patent No. 6559297
GENERAL INFORMATION:
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                                                                                    AATCCGGAGTGCACAGAAGAAGAAGCTCTAAGTCATGTTTATGGTATCATCGACAACGCA
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NAME/KEX: CDS
CACATLON: (2)...(2347)
OTHER INFORMATION: E-alpha-bisabolene synthase
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US-09-003-012B-45

Sequence 45, Application US/09903012B

Sequence 45, Application US/09903012B

Sequence 45, Application US/09903012B

Patent No. 6566565

APPLICANT: Chappell, Joseph

APPLICANT: No. 6566561, Joseph P.

APPLICANT: Manna, Katheen R.

TITLE OF INVENTION: SYNTHASES

FILE REFERENCE: 07678-02501

CURRENT APPLICATION NUMBER: 00/100, 993

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 3.0

SENGTH: 2424
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	1691 TTCAATATGGTGCAGGCCTTACACCAAAAGAGAGACTCAACACATTGTCAGCTGGTGGAGA 1750 	1751 GAATGGGGATTCAATGATTTACACCGCCAGCGGCCTGTGGAAATGTATTCTCA 1810	1811 GTGGCGGTTAGTATGTTTGAGCCAGAATTCGCTTGTAGAATTGCCTATGCCAAGACT 1870	TCTTGCCTCGCAGTTATTCTAAGACGATCTTTACGACCCCCCGCGATCTCTGGATGATCTT	1931 AAATTGTTCTCTGAAGGTCCGAAGATGGGATATCTCTGTGTGCATAGCGTTCGGGAT 1990 		2051 GGACTCAAGGAACAAGGCCGTGATGTGGTGGGTATCTTCGAAAAGTATGGGAGGGTTG 2110 	2111 CTGGCATCGTATACCAAAAGCCGAATGGTCGGCAGCAAAGTATGTGCCGACATTCAAC 2170 	GAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCAATC	2231 TTTTCACTGGAGATTACTTCCTGATTACATTTTACAGCAGTAGACCTTCGGTCC 2287	AAATTTCTGCATCTTGTGTCTTTGACTGGACGACTAATGACACGAGACT 	2342 TACCAGGCCGAGAGAACCGTGGTGATTGGTTTCCAGGGTACAGTGCTACATGAGGGAA 2401 	2402 AATCCGGAGTGCACAGAGGAAGAAGCTCTAAGTCATTTATGGTATCATCGACAACGCA 2461 	2462 CTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGGAGCAATGCCCCATTGTGTGTG	2522 AGACTGCTGTACACTGCAAGAGTGATGCAGCTGTTTTATATGTACAGAGATGGCTTT 2581	2582 GGTATCTCTGACAAAGAGATGAAAGACCATGTCAGCGGAACTCTTTCGATCCTGTGGCG 2641	2642 TAGCATACTGATATTATATATATATATTCATATTCATATTCAAAAAAA 2688 	2689 AAAAAAAAAAAAAA 2705
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1871 TCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACACCCACGGATCTCTGGATGATCTT 1930
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Pred. No. 8.2e-210;
0; Mismatches 893;
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; OTHER INFORMATION: E-alpha-bisabolene synthase US-09-900-797-45
                                                                                               US-US-900-797-95
1 Sequence 45. Application US/09900797
2 Patent No. 6645762
3 GENERAL INFORMATION:
3 APPLICANT: Chappell, Joseph
3 APPLICANT: Chappell, Joseph
4 APPLICANT: Starks, Courtney M.
5 APPLICANT: Manna, Kathleen R.
7 ITILB OF INVENTION: SYNTHASES
7 FILE REPERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395
PRIOR APPLICATION NUMBER: US/09/398,395
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FEBSESEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 45
2405 AAAAAAAAAAAAAA 2421
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Best Local Similarity 59.6%;
Matches 1370; Conservative
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                                                                  GAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCAATC 2230
                                                                              2108 CATCCTGAATGTACAGAGGAAGAGGCTCTCGATCACATCTATAGCATTCTGGAGCCGGCG 2167
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Sequence 77, Appl
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Sequence 29, Appl
Sequence 27, Appl
Sequence 57, Appl
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Sequence 397, Application Wo. US2004007232341
Septembral Information:
APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
FITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080USS/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT PILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 397
LENGTH: 2705
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US-10-025-145A-15
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        TYPE: DNA; ORGANISM: Ginkgo biloba
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1. /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2. /cgn2_6/ptodata/1/pubpna/DFT_NEW PUB.seq:*

3. /cgn2_6/ptodata/1/pubpna/US06_DNEW PUB.seq:*

4. /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5. /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

6. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8. /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9. /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*

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                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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18 US-10-041-007-34

18 US-10-041-007-36

18 US-10-041-007-36

18 US-10-041-007-38

18 US-10-041-018-365

18 US-10-08-365

18 US-10-08-365
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APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Schepmann, Hala G.
ITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase; PILE REFERENCE: PO2081US1; CURRENT APPLICATION NUMBER: US/10/041,007; CURRENT FILING DATE: 2002-01-07; PRIOR APPLICATION NUMBER: US 60/259,881; PRIOR PILING DATE: 2002-01-07; PRIOR PILING DATE: 2001-01-05; NUMBER OF SEQ ID NOS: 41; SEQ ID NOS: 41; SEQ ID NO: 17, TENERAL PARENTIN VERSION 3.1
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Best Local Similarity 100.
Matches 2705; Conservative
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; ORGANISM: ginkgo biloba
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Sequence 34, Application US/10041007

Sequence 34, Application US/10041007

Publication No. US20020164736A1

GENERAL INFORMATION:
APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Schepman, Hala G

TILLE OF INVENTION: Glinkgo Biloba Levopimaradiene Synthase;
FILE REFERENCE: P02081US1:
CURRENT APPLICATION NUMBER: US/10/041,007

CURRENT APPLICATION NUMBER: US 60/259,881

PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR PILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 3.1

SEQ ID NO 34

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90.3%; Score 2442; D
Best Local Similarity 100.0%; Pred. No. 0;
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US-10-001-36

Sequence 36, Application US/10041007

Sequence 36, Application US/10041007

Publication No. US20020164736A1

GENERAL INFORMATION:

APPLICANT: Schepman, Hala G

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

FILE REFERENCE: PO20B1US1

CURRENT APPLICATION NUMBER: US/10/041,007

CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR PILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PALENT Version 3.1

SEQ ID NO 36
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; ORGANISM: Ginkgo biloba
US-10-041-007-36
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Sequence 38, Application US/10041007
Fublication No. US20020164736A1
GENERAL INPORMATION:
APPLICANT: Matusda, Selichi P.T.
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase;
FILE REFERENCE: PO2031US1
CURRENT FILING DATE: 2002-01-07
PRIOR PAPLICATION NUMBER: US/10/041,007
CURRENT FILING DATE: 2002-01-07
PRIOR PAPLICATION NUMBER: US 60/259,881
TURE: DAS OF SEQ ID NOS: 41
SEQ ID NO 38
IENGTH: 2241
TYPE: DAS OGGANISM: Ginkgo biloba
US-10-041-007-38
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2241; Conservative 0; Mismatches 0;
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US-10-041-007-38
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944 TCAAGAGAGGGATCATTTTTAAGCTCCCCTGCATCTACTGCTTGTGTCTTCATGCACACT 1003	1004 CAAAACAAACGATGCCTCCACTTTCTCAACTTCGTGCTCAGCAAATTTGGGGACTACGTT 1063 		TTGGGAATCGATGGCTATTTCAAGAAAGAAATCAAAGAATCTCTGGATTACGTTTATAGG 	1184 TACTGGGACGCCGAAAGAGGCGTGGGATGGGCAAGATGCAATCCTATTCCTGATGTCGAT 1243 	1244 GACACTGCCATGGGTCTTAGAATCCTGAGACTTCATGGATACAATGTATCTTCAGATGTT 1303 	1304 CTGGAGAATTTCAGAGAGAGAGAGAGAGTTCTTTTGCTTTGCCGGTCAAACGCAAATT 1363	1364 GGTGTGACCGATAATCTTAACCTTTATAGATGTTCACAAGTATGTTTTCCGGGAGAAAG 1423 	1424 ATAATGGAAGAAGCTAAGACCTTCACTACAAATCATCTCCAAAATGCTCTTGCCAAAAC 1483 	1484 AACGCATTTGATAAGTGGGCTGTCAAGAAGGATCTTCCTGGAGAGTGGAGTATGCTATA 1543 	AAGTATCCGTGGCATAGAAGTATGCCAAGATTGGAGGCAAGAAGTTACATAGAGCAATTT 	1604 GGATCAAATGATGTCTGGCTGGGGAAGACTGTGTATAAGATGCTATATGTGAGCAACGAA 1663 	1664 AAATATTTGGAGCTGGCCAAATTGGACTTCAATATGGTGCAGGCCTTACACCAAAAGGAG 1723 	1724 ACTCAACACTTGTCAGCTGGAGAGAATCGGGATTGAATGATTACATTCACCGG 1783 	1784 CAGGGGCTGTGGAAATGTATTTCTCAGTGGCGGTTAGTATGTTTGAGCCAGAATTCGCT 1843 	1844 GCTTGTAGAATTGCCTATGCCAAGACTTCTTGCCTCGCAGTTATTCTAGACGATCTTTAC 1903 	1904 GACACCCACGGATCTTCTGATGATCTTAAATTGTTCTCTGAAGCGGTCCGAAGATGGGAT 1963 	1964 ATCTCTGTGCTGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTAC 2023

US-09-887-586A-55		ò	1370 ACCGATAATCTTA
Query Mat. Best Loca.	; Length 2861;	qq	1 1341 ACAGACATGTTAA
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AAATCCGGAGTGCACAGAGGAGGAGGCTCTAAGTCATGTTATGGTATC 2449 TGGTGGAGAATCGGGATTCAATGATCTTACATTCACCGGCAGCGG GGAAAAGGTGGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTT GITCGGGAIAATCAGITGAAAGITIGCIICCIAGGGCIGIACAACACA CGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTAATCAAT ACCTITATAGATGTTCACAAGTATGTTTCCGGGAAAAAAAATG GCTTTTAAAAGAATATTCGGGGAGAGGTAGAGTATGCACTCAAATAT GCTGTCAAGAAGCATCTTCCTGGAGAGGGGAGAGGGAGTATGCTATAAAGTAT

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Patent No. US20020094557A1
GERREAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Rarks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
ITHLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012
CURRENT APPLICATION NUMBER: 09/398,395
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
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Sequence 55, Application US/09900797
Publication No. US20030087406A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20030087406A11, Joseph
APPLICANT: Starks, Courtney M.

US-09-900-797-55

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AAACGAIGCCICCACTITCICAACITCGIGCICAGCAAATITGGCGACTACGITCCIIGC 1069
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40.3%; Score 1091.4; DB 10; Lengt
Best Local Similarity 68.4%; Pred. No. 0;
Matches 1574; Conservative 0; Mismatches 713; Indels
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/900,797
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-08-22
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTESEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 2861
                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS; (2606)
COTHER INFORMATION: abietadiene synthase
US-09-900-797-55
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ORGANISM: Abies grandis
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; Bublication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Selichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TILE OF INVENTION: Diterpene-Producing Unicellular Organism; FILE REPRENCE: P020800171/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; RUBMER OF SEQ ID NOS: 413
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Best Local Similarity 68.4%; Pred. No. 0;
Matches 1574; Conservative 0; Mismatches 713; Indels
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SEQ ID NO 365 .
LENGTH: 2861
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US-10-041-018-365
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AAAAAGTGCTTGGATTTCTTGAACTTTGTCTTGAAGAAATTCGGAAACCATGTGCCTTGT 1043
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RESULT 11
US-09-893-820-55
Sequence 55, Application US/09893820
Publication No. US20040053386A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Coutrney M.
APPLICANT: Bana, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REPERENCE: 07679-025001
CURRENT FILING DATE: 2001-06-28
PRIOR PPLICATION NUMBER: US/09/893,820
CURRENT FILING DATE: 1999-017
PRIOR PILING DATE: 1999-017
PRIOR PILING DATE: 1999-017
PRIOR PILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ 1D NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEC 1D NO 55-
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40.3%; Score 1091.4;
Best Local Similarity 68.4%; Pred. No. 0;
Matches 1574; Conservative 0; Mismatches
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NAME/KEY: CDS

LOCATION: (3)...(2606)

OTHER INFORMATION: abletadiene synthase
US-09-893-820-55
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Pred. No. 0;
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Query Match
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; OTHER INFORMATION: B-alpha-bisabolene synthase
US-09-887-586A-45
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APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: U9/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-08-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/09887586A Patent No. US20020094556Al GENERAL INFORMATION:
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US-09-887-586A-45
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GENERAL INFORMATION:
APPLICANT: No. US20020094557A11, Joseph P. APPLICANT: Starks, Courtney M. APPLICANT: Manna, Kathleen R. TITLE OF INVENTION: SYNTHASES; FILE REFERENCE: 07678-025001; CURRENT APPLICATION NUMBER: US/09/903,012; CURRENT FILING DATE: 2001-07-11; PRIOR FILING DATE: 1999-09-17
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                                                                                                                                                                                                                                                                         Length 2424;
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LOCATION: (2)...(2347)
OTHER INFORMATION: E-alpha-bisabolene synthase
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR PLING DATE: 1999-04-22
PRIOR PLING DATE: 1999-04-22
PRIOR PRIOR DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE PARESE PARESEQ for Windows Version 3.0.
LENGTH: 2424
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ORGANISM: Abies grandis
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COTHER INFORMATION: E-alpha-bisabolene synthase
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US-09-900-797-97

Publication No. US20030087406A1

GENERAL INFORMATION:

APPLICANT: Chappell, Joseph

APPLICANT: Cappell, Joseph

APPLICANT: Earks, Courtney M.

APPLICANT: Manna, Kathleen R.

TITLE OF INVENTION: SYNTHASES

FILE REFERENCE: 07678-02501,

CURRENT FILING DATE: 2001-07-06

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: 60/130,628

PRIOR PLING DATE: 1999-09-17

PRIOR PLING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: 60/130,628

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: 60/150,262

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FRASESEQ for Windows Version 3.0

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GenCore vergion 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd OM nucleic - nucleic search, using sw model Run on: August 24, 2004, 06:59:45; Search time 6	Title: Perfect score: 2705 Sequence: 1 atatttgcctaaacctgcacaaaaa Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters:		6: em estpl:* 7: en_estro:* 8: en_htc:* 9: gb_estl:* 10: gb_est2:* 11: gb_htc:* 12: gb_est3:* 13: gb_est4:* 14: gb_est5:* 15: en_estfun:*	16: em_estom:* 17: em_gss hum:* 18: em_gss inv:* 19: em_gss inv:* 20: em_gss vrt:* 21: em_gss_fun:* 21: em_gss_fun:* 23: em_gss_mam:* 24: em_gss_pro:* 25: em_gss_pro:* 26: em_gss_pro:* 26: em_gss_vrt:* 27: em_gss_vrt:* 29: ep_gss_vrt:* 29: ep_gss_vrt:*	the r than than ry ch Le

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1035 TCGTGCTCAGCAAATTTGGCGACTACGTTCCTTGCCATTACCCACTTGATCTATTTGAAC 1094
University of Florida, sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: JENREV (CAGGAAACAGCTATGACC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aracricrcraracegriccaacaararacricrarrarriscaacecriccaacaarae 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGACTGGCAAGAGATCACAAATCTTCAATCAAGAGACGGATCATTTTAAAGCTCCCTG 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 ITGICITICCIGCIAIGCIAAGGAAGCAATIAIGCTIGGAICIGCCITAIGAGI 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCCTTTCATCTCCCAAAATCCACAAAAGCGCCAGAAAAAGCTTCAAAAAGATTCCCCTCA 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcracaecegererarreareceracaeggaacaceaagreerregaarrerreaacr 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 ĠĠĠĠīĠAAĠAcAAĊCAŤŤŗĊĊŤAAGAŤAŤĠĀĊĀĠĀĠŤACŤĊĀĊŢĀĊŤŢŢĠĊĠŢĠŢĀŤŦA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 TCACTCTCAAAATATGGAATAAGGGCGACATTCAAGTGCAGAAAGGGGGTTGAGTTTGTGA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        675 GAAAACACATGGAAGAAATGAAGGACGAAGCTGACAATCACAGGCCAAGTGGATTCGAGG 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCAGACATTGGTGAAGGAAATCCAGTGCATGTTTCAGTCCATGGGCGACGGTGAAACGA 434
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                                                                                                                                                                                                                                                                                                                                           /Bright Publish (1970) | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1972 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 1973 | January 197
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14.1%; Score 380.8; DB 14; Length
Best Local Similarity 68.5%; Pred. No. 8e-57;
Matches 526; Conservative 0; Mismatches 242; Indels
                                                                                                                                                                                                                                                         /organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555
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/dev stage="adult"
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/note="Vector: Uni-Zap XR lambda (Stratagene); Site l: Eco
RI; Site 2: Xho I; A composite cDNA library was made with
mRNA isolated from normal, compression, opposite, early
and late wood of Maritime pine uni-directionally cloned
into Uni-ZAP XR using the ZAP-CDNA Synthesis kit
(Stratagene). pBluescript SK(-) plasmids were obtained by
in vivo mass excision. The nuclectide sequence of the
s'end was obtained by automated sequencing with the T3
primer by GENOME EXPRESS, Meylan, France"
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                                                                                                                                                                                                                                                                                                      BX682869 Binus pinaster differenciating xylem adult Pinus pinaster cDNA clone 122H09 similar to Pinene synthase (EC 4.2.3.1), mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinus, Pinus,
1 (Dases 1 to 730)
Canton,F.R., Le Provost,G., Garcia,V., Barre,A., Frigerio,J.-M.,
Paiva,J., Fevereiro,P., Avila,C., Mouret,J.-F., Brach,J., de
Parauvar,A., Canovas,F.M. and Plomion,C.
Transcriptome analysis of wood formation in maritime pine
Unpublished (2003)
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Gaps
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                                                                                            771
                                                                                                                                route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .730
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/db_xref="taxon:71647"
/clone="122H09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Frigerio JM
Genetique et Amelioration 69
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ecrcrecaegarerecarecriricacaariececerraaaaagaarcrireeeceadae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 AATGTTTTCAACGAAAATATTTGGAATTAGCAAAATTGGATTTCAATCGACTGCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTACATTCACCCGCCAGCGGCCTGTG---GAAATGTATTTCTCAGTGGCGGTTAGTATG
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Cother ESTS: RTWW2 13 C12.bl A021
Cother ESTS: RTWW2 13 C12.bl A021
Cother Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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RNA prepared and library constructed by W. Walter Lorenz, School of

Porestry, University of Georgia; plant material prepared at the

Porestry, University of Georgia; plant material prepared at the

University of Florida; sequencing done in the Laboratory for

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.

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                                                                ATGGATTTGGAAAAGATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAA
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Submitted (15-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.isatate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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Pred. No. 1.3e-36;
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RNA prepared and library constructed by W. Walter Lorenz, School of
Foreerry, University of Georgia; plant material prepared at the
Foreerry, University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREY (CAGGAAACAGCTATGACC).
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Pratt., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and
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An EST database from drought-stressed loblolly pine (Pinus taeda)
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 228.8; DB 14; Length 725; Pred. No. 3.2e-30;
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Tel: 919 515 7800
Fax: 919 515 7801
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Please see http://web.ahc.umn.edu/blodata/nsfpine/ for further
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Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000)
Contact: Sederoff. Ron
Forest Biotechnology
North Carolina State University
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                                                                                                                                                                                                                                                                                                                                                                                               /close libe "RS".
/close libe "RS".
/close "Vector: Uni-ZAP XR; ecotype: Landes; The library made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmetic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dr primed cDNA was directionally cloned into the EcoRI-Xhol lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"
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                                                                                                                                                                                                                                                                               /tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
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                         Location/Qualifiers
1. .583
/organism="Pinus pinaster"
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Frigerio, J. and Plomion, C.
Indentification of water-deficit responsive genes in Maritime pine (Pinus pinaeter Ait.) using an EST approach
                                                                                                                                                                                                                                                     1593 TAGAGCAATTTGGATCAAATGATGTCTGGCTGGGGAAGACTGTGTATAAGATGCTATATG 1652
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Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
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Genetique et Amelioration 69
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2151 AGTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCATAG 2201
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Other ESTB: RTDS1 17 C03.bl A015
Contact: Cordonnier-Pratt MM
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/lab_host="RTD53 23 G06 A022"
/lab_host="RTD53 23 G06 A022"
/lab_host="RTD54 I plage-resistant E. coli"
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library was prepared from poly4+ RNA from drought-stressed
loblolly pine (Pinus taeda) roots. Water was withheld from
ramet clones until predawn needle water potential reached
-1.75 MPa. On day 7 roots were harvested for RNA
isolation. Double-stranded CDNA was cloned
unidirectionally into pSL1180. Inserts excised with EcoRI
(5' end) and Xho1 (3' end)."
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Porestry, University of Georgia; plant material prepared at the Porestry, University of Georgia; plant material prepared at the Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAAACAGCTATGACC).
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Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
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An EST database from drought-stressed loblolly pine (Pinus taeda)
                                                                                                                                                                                                                                                                                   Other_ESTS: RTDS3_23_G06.bl_A022
Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
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60.4%; Pred. No. 4.2e-26; .
ive 0; Mismatches 231; Indels 3;
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                                             Pinus taeda (loblolly pine)
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    GI:34356363
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/lone lib="Drought-stressed loblolly pine roots DS1"
/note="vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from pol/A+ RNA from drought-stressed
loblolly pine (Pinus taeda) roots. Water was withheld from
ramet clones until predawn needle water potential reached
1.75 MPa. On day 7 roots were harvested for RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into pSL1180. Inserts excised with EcoRI
(5' end) and XhoI (3' end)."
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RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JURISY (CAGGAAACAGCTATGACC).
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1971 TGCTGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTACAACACAG 2030
                                                                                           369 ATACGGAAAACCTTCCAGACTATA---TGAAGCTATGTTACAAAATCTATTATGACATAG 425
                                                                                                                                                                                                                                                     TTCACGAAGTGGCCTGGGAGGCAGAGAAGAAAGGAACGGGACGTGAATTACTTAGCTTTTTCA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 GAAAGGGATGGGATTATCTTCTGGGTTATTATGAAGAAGCTGAATGGCTAGCAGCTG 545
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An EST database from drought-stressed loblolly pine (Pinus taeda)
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Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tal: 706 542 1860
Fax: 706 583 0210
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2207 GCGACAGTCGTACTAAACTCAATCTTTTCACTGGAGAATTACTTCCTGATTACATTTA 2266
                                                       Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of

RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-prime sequences are presented as their reverse complement

and have been trimmed to exclude polyA.

Seq primer: JENREY (GAGGAAACAGCTATGACC).
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7.1%; Score 190.8; DB 14; Length
Best Local Similarity 55.6%; Pred. No. 1.4e-23;
Matches 388; Conservative 0; Mismatches 307; Indels
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THING T BIL. GL A021 Well-watered loblolly pine roots WW2 Pinus taeda cDNA clone RIWW2_7_B11_A021 5', mRNA sequence.
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Spermatophyta; Coniferopaida; Coniferales; Pinaceae; Pinus, Pinus.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J.
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                                         Score 204.4; DB 14; Length
Pred. No. 5.9e-26;
0; Mismatches 256; Indels
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CETULE BOS. 91 A015 Well-watered loblolly pine roots WW1 Pinus taeda CDNA clone RTWW1_15_BOS_A015 5', mRNA sequence.
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
                         121 GACAGAGTGCCTTCCAGAATATATGAAAGGAGTTTACATGATAG---TTTACAACACTGT
                                                                                                         178 APATGABATGTCTCAGGAGGCAGACAAGGCTCAAGGCCGAGACACGCTCAACTATTGTCG
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  GCTGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTACAACACAGT
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Other EST9 arm well-watered loblolly pine (Pinus taeda) roots
Unpublished (2003)
Other EST9 xTWW3 5 A06.D1 A02.
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Pax: 706 583 10210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmprattwing.edu
RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
TGCTACATGAGGGAAAATCCGGAGTGCACAGAGGAAGAAGCTCTAAGTCATGTTTATGGT 2446
                                                                                                                                                                                                                        CF477103

RTWW3_S_A06.g1_A022 Well-watered loblolly pine roots WW3 Pinus read a cDNA clone RTWW3_S_A06_A022 5', mRNA sequence.
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                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. I tabbese 1 to 745)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, M.W., Dean, J., Gebremednin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
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7.0%; Score 190.4; DB 14; Length 745;
Best Local Similarity 54.8%; Pred. No. 1.7e-23;
Matches 399; Conservative 0; Mismatches 326; Indels 3;
                                                                                  2447 ATCATCGACAACGCACTGAAGGAATTGAATTGGGAGTT 2484
                                                                                                         ATGGTCGATAACTTAACCAAGGAACTGAATTGGGAGTT 696
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Pinus taeda
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/clone="RTWW1 15 B05 A015"
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/clone lib="Well-watered lobiolity pine roots WW1"
/clone lib="Well-watered lobiolity pine roots WM1"
/note="Vector: pSi1180; Site 1: ECORI; Site 2: Xhoi; The library was prepared from polyA+ RNA from lobiolity pine (Finus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSi1180. Inserts excised with ECORI (5' end) and Xhoi (3' end)."
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         Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polya. Seq primer: JENESY (CAGGAAACAGCTATGACC).
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mRNA linear EST 28-OCT-2003 clone RN41G08, mRNA sequence.
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                                                                                                                                                                                                 Pinus pinaster

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus, Pinus.

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1 (binus pinaster Ait.) using an EST approach
Contact: Frigerio JM
Genetique et Amelioration 69
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hote="Vector: Uni-ZAP XR; ecotype: Landes; The library
hat made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A mixture of genotypes were used.
oligo-dr primed cDNA was directionally cloned into the
ECORI-*ADI lambda-ZAP vector arms and mass-excised to for
a pBluescript phagemid"
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Best Local Similarity 64.9%; Pred. No. 1.1e-22;
Matches 292; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="root"
/dev_stāge="6 weeks old seedling"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           route d'Arcachon 33612 Cestas CEDEX
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
      581 bp
BX677559 RN Pinus pinaster cDNA
BX677500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
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                                                                     BX677599
BX677599.1 GI:38011551
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1562 AGTATGCCAAGATTGGAGGCAAGAAGTTACATAGAGCAATTT---GGATCAAATGATGTC 1618
                                                   1262 AGAATCCTGAGACTTCATGGATACAATGTATCTTCAGATGTTCTGGAGAATTTCAGAGAC 1321
                                                                                                                                             1322 GAGAAAGGAGACTTCTTTTTGCCTGTCAAACGCAAATTGGTGTGACCGATAATCTT 1381
                                                                                                                                                                                                                                        1382 AACCTTTATAGATGTTCACAAGTATGTTTTCCGGGAGAAAAGATAATGGAAGAAGGCTAAG 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1619 TGGCTGGGGAAGACTGTGTATAAGATGCTATATGTGAGCAACGAAAAATATTTGGAGCTG 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA223665
SCJFFL1C04F02.g FL1 Saccharum officinarum cDNA clone SCJFFL1C04F02
                                                                                   188 CGCTGCTGCCGCTTCATGGATACGATGTCTCCCCAAGTGTATTTGGGAAGTF---TGAG 244
                                                                                                                                                                                                                                                                                                                                    1442 ACCTTCACTACAAATCATCTCCAAAATGCTCTTGCCAAAAACAACGCATTTGATAAGTGG 1501
                                                                                                                                                                                                                                                                                                                                                                                                                            1502 GCTGTCAAGAAGGATCTTCCTGGAGAGGTGGAGTATGCTATAAAGTATCCGTGGCATAGA 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 AACCTGAACAGGGCCTCTCAGGTAAGGTTCCCTGGAGGACTTGTTGCAGCGTGCAGGG 364
                                                                                                                                                                                                                                                                                                                                                                              365 AGATICICGIAIGAGITCCITAGAGAAAGGGAAGCCCAIGGCACGAITCGAGACAAAIGG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 ATCATTGCTAAGGATCTACCAGGCGAGGTAAAATATACACTGGACTTCCCATGGTATGCA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AAGGACGGGGAGTTCTTCTTCTTCGTGGGCAATCAACACAAGCAGTCACTGGGATGTAC 304
  128 GGGATTTGCTGGGCGAGGAACTCCACTGTAATAGACGTGGATGATACATCCATGGCATTC 187
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: CO4 row: F column: 02
Seg primer: T7 Promoter Primer.
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/lab_host="DH10B"
/clone_lib="FL1"
/note="Organ: Inflorescence at begining of development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kemper, E.L. and Arruda, P.
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Saccharum officinarum
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CA223665
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F-PRIME, mRNA sequence.
BU971902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone libe "BC"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); developing caryopsis, $6.15 DAP(days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, PStI).
NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 624)
Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
Contact: Stein Nils
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensetr. 3, 06466, Gatersleben, Germany
Tel: 039482-5595
Fax: 039482-5595
Email: Stein@ipk-gatersleben.de
Insert Length: 624 Std Error: 0.00
Plate: 20 row: A column: 6
Seg primer: Mi3rev.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="developing caryopsis"
/dev stage="8-15 DAP (days after pollination)"
/lab_host="XLI0-Gold"
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|cultivar="barke"
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                                                                                                      552 ATGTGCCCTCCTTCAATGAATACATAGAGA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /aub_species="vulgare"
/db_xref="GABI:236738"
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Matches 368; Conservative
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1574 TTGGAGGGAAGAAGTTACATAGAGCAATTTGGATCAA---ATGATGTCTGGCTGGGGAAG 1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCAATATGGTGCAGGCCTTACACCAAAAGGAGACTCAACACATTGTCAGCTGGTGGAGA 1750
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An unidirectional cDNA library generated from Unidirectional cDNA library generated from [Inflorescence at begining of development (ice-long)]. cDNA was prepared from polyA+mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sixing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 ACCCTATACAGGATGCCTCTTGTGAATAACGACATATATCTTGATTTTGGCATAATGGAT 535
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6.8%; Score 184.2; DB 14; Length
Best Local Similarity 57.1%; Pred. No. 2.1e-22;
Matches 396; Conservative 0; Mismatches 288; Indels
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Search completed: August 24, 2004, 15:24:14 Job time : 6852.72 secs

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us-10-041-007-2.rag

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GenCore version 5.1.6
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- protein search, using sw model OM protein

August 17, 2004, 20:53:08; Search time 54.4614 Seconds (without alignments) 4529:153 Million cell updates/sec Run on:

US-10-041-007-2 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum 1 Maximum 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* Database

genesequ1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003bs:* geneseqp2003bs:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abu09779 Maidenhai	Aay90858 Grand fir	Abb79393 Taxadiene	Abu09780 White fir	2	2 Grand	Abu09781 White fir	_		-		Grand	Aab69373 Grand fir	Abb79392 Taxadiene	Aaw31655 Pacific y	Aay90852 Yew taxad	-	Abu09782 Pacific y	Aay84104 Soybean c	Aae24916 Soybean c	Aar90848 Gibberell	Abb92819 Herbicida	Aar93800 Anther ea	Aay06569 Delta-sel	Aay06571 Delta-sel
dī	ABU09779	AAY90858	ABB79393	ABU09780	AAY06567	AAY06562	ABU09781	AAY06566	AAY06568	ABB79391	AAW85703	AAY90853	AAB69373	ABB79392	AAW31655	AAY90852	ABB79394	ABU09782	AAY84104	AAE24916	AAR90848	ABB92819	AAR93800	AAY06569	AAY06571
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% Query Match	100.0	61.2	61.2	60.8	45.5	45.5	45.5	45.5	45.5	45.5	44.9	44.9	44.9	44.9	42.2	42.2	42.2	42.2	29.7	29.7	28.7	28.7	28.4	27.0	27.0
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ALIGNMENTS

Levopimaradiene synthase; ginkgolide; enzyme; Escherichia coli; Candida albicans; Kluyeromyces lactis; Saccharomyces; maidenhair tree. Maidenhair tree levopimaradiene synthase. ABU09779 standard; protein; 873 AA. 07-JAN-2002; 2002US-00041007. 05-JAN-2001; 2001US-0259881P. Matsuda SPT, Schepmann HG; 06-AUG-2003 (first entry) (MATS/) MATSUDA S P T. (SCHE/) SCHEPMANN H G. WPI; 2003-352584/33. JS2002164736-A1 Ginkgo biloba. 07-NOV-2002. ABU09779; ABU09779

New purified and isolated nucleic acid sequence encoding a levopimaradiene synthase useful for producing pure ginkgolides in cells.

Claim 20; Fig 4; 37pp; English.

The invention relates to a purified and isolated nucleic acid sequence encoding a levopimaradiene synthase. The nucleic acid is used for the preparation of a ginkgolide in a cell, an expression vector, a unicellular organism (e.g. Saccharomyces, Escherichia coli, Candida albicans or Kluyeromyces lactis), a yeast host cell, a plant (particularly Ginkgo biloba), a host cell, a transgenic plant or a seed of the transgenic plant, for the biosynthesis of ginkgolides and in molecular biology, molecular genetics, and organic chemistry. The nucleic acid is capable of producing large amounts of pure ginkgolides in a costeffective manner, particularly in an organism capable of a high-yield sinkgolide-producing system. This sequence represents a levopimaradiene synthase polypeptide of the invention

(first entry)

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Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
                               Synthase; protein co-ordinate data; active site; modification; terpenc 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antimour; ateroid hormone; signal transduction pathway; bile acid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent.
              Grand fir abietadiene synthase protein sequence SEQ ID NO:56.
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N-PSDB; AAA38937.
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25-AUG-2000
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23-AUG-1999;
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100.0%; Pred. No. 0;
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Starks CM;

Manna KR, Noel JP,

KENTUCKY RES DEPT 99US-0130628P.

99WO-US021419 98US-0100993P

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The present invention describes an isolated terpene synthase (I)

Comprising a region with at least 20% identity to region 265-535 of a 548

comprising a region with at least 20% identity to region 265-535 of a shall an early a sequence (la), given in AAY90811. (I) contains nine alpha carbon atoms (alphaC) that have interactomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom) within tabulated arange, and have an ordered arrangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and cralted enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precusors of steroid confidence of signal transduction pathways, precusors of steroid confidence components of signal transduction pathways, precusors of steroid confidence of signal transduction pathways, precusors of steroid confidence of signal transduction pathways, precusors of steroid confidence of signal transduction pathways, precusors of steroid confidence of signal transduction pathways, precusors of steroid concounts them) are used as controls in the analysis of products formed by encoding them) are used as controls in the analysis of produces or develop immunological reagents or nucleic acids for monitoring expression of terpene synthases or inheritance of the gene in controls. AnAssalo to AnAssals and Anysousl to ANASSASO to ANASSASO to conducts. ANASSASO to Exemplification of the present invention
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Best Local Similarity 62.3%; Pred. No. 1.9e-248;
Matches 546; Conservative 120; Mismatches 183; Indels 2
Claim 112; Page 443-445; 450pp; English.
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AAY90858 standard; protein; 868

AAY90858

AAY90858 ID AAY9 XX AC AAY9 XX

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2000DK-00001730

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Heterologous production of taxane analogs related compound useful as anticancer agent involves cloning a full-length taxane synthesis pathway from a taxan-producing organism into a taxane-resistant host cell.
                                                                                                       Example 3; Fig 1; 60pp; English.
16-NOV-2001; 2001WO-DK000763
                                                              VPI; 2002-471624/50
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                                                                                        VDWQEITNLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFE 357
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              VVPPAMLDEAKSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDV
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The present invention describes the heterologous expression of taxane analogues, comprising cloning a DNA sequence comprising a taxane synthesis pathway, making a DNA construct in which the DNA sequence is under control of regulatory elements, introducing the DNA construct into a host cell, growing the host cell to produce taxane analogues, and recovering the required taxane from the culture medium. Also described: (1) an isolated DNA sequence comprising the taxane synthesis pathway, (preferably taxol synthesis pathway); (2) an expression vector comprising that isolated DNA sequence; and (3) a host cell comprising a taxane synthesis pathway derived from a taxane-producing organism, plant or tree, the taxane synthesis pathway is foreign to the host cell. The taxane analogues have cytostatic activity, and so can be used as an analogues have cytostatic activity, and so can be used as an analogues protein, which is given in an example from the present
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llarity 62.3%; Pred. No. 1.9e-248;
Conservative 120; Mismatches 183;
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Matches 546; (
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537

478

taxane synthesis; taxadiene synthase; cytostatic; anticancer;

WO200240694-A2

23-MAY-2002

Unidentified

Taxane;

Taxadiene synthase homologous protein sequence q38710

(first entry)

13-AUG-2002

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a purified and isolated nucleic acid sequence encoding a levophmaradiene synthase. The nucleic acid is used for the preparation of a ginkgolide in a cell, an expression vector, a unicellular organism (e.g. Saccharomyces, Escherichia coli, Candida albicans or Kluyeromyces lactis), a yeast host cell, a plant (particularly Ginkgo biloba), a host cell, a transgenic plant or a seed of the transgenic plant, for the biosynthesis of ginkgolides and in molecular biology, molecular genetics, and organic chemistry. The nucleic acid is capable of producing large amounts of pure ginkgolides in a cost-effective manner, particularly in an organism capable of a high-yield
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levopimaradiene synthase useful for producing pure ginkgolides in cells.
                                                   AVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDN
                                                                                                  RNRGELVSSVOCYMRENPECTEEEALSHVYGIIDNALKELNWELANPASNAPLCVRRLLF
                                                                                                                                                                        RYLRNALENVDAFDKWAFKKNIRGEVEYALKYPWHKSMPRLEARSYIENYGPDDVWLGKT
                  VYKMLYVSNEKYLELAKLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSV
                           QLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNE
                                                                                                                                                                                                                                                                                                                                      Levopimaradiene synthase; ginkgolide; enzyme; Escherichia coli;
Candida albicans; Kluyeromyces lactis; Saccharomyces; white fir;
abietadiene synthase.
                                                                                                                                                                                                             NTARVMOLFYMYRDGFGIS-DKEMKDHVSRTLFDPVA 873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 4; 37pp; English
                                                                                                                                                                                                                                                                   ABU09780 standard; protein; 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-2002; 2002US-00041007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTVXKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRORFVEMYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 SVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVR
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                                                                                                                                                                                                                                                                                                                                                                                                           HASAAETRPDQLPQEERFVSR---LNADYHPAVWKDDPIDSLTSPNSHATSKSSVDETIN
                                                                                                                                                                                                  GSWGEECIFLAYDRYLNTLACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSG
                                                                                                                                                                                                                                                                                                   174 GSWGEGFYFLAYDRILATLATLATLTLTLWRTGETQVQKGIESFRTQAGKWEDEADSHRPSG
                                                                                                                                                                                                                                                                                                                                                          DVVDWQEITNLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDL
                                                                                                                               SLOLSPXVP----FROSTNILIPFHKRSSFGFNAQHCVRSHLRLRWN-----CVGI
                                                                                                                                                      5 SSSLSSQIPTAAHHLTANTQSIPHFSTTLNAGSSASK--RRSLYLRWGKGSNKIIACVG-
                                                                                                                                                                                                                                   KRIQILVKRIQCMFQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPD
ginkgolide-producing system. This sequence represents an abietadiene synthase polypeptide which shows similarity to the levopimaradiene synthase of the invention
                                                                                                          32;
                                                                               Length 868;
                                                                               Query Match 60.8%; Score 2825; DB 6; Length 8
Best Local Similarity 61.8%; Pred. No. 1e-246;
Matches 543; Conservative 124; Mismatches 180; Indels
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SGVLIMDGQLLSQEALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASSIECY
                                                                                                                                                        FKKE1KESLDYVYRYWDAERGVGWARCNP1PDVDDTAMGLR1LRLHGYNVSSDVLENFRD
                                                                                                                                                                                                                                434 EKGDFPCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMBEAKTFTTNHLQNALAKNNAFDKW
                                                                                                                                                                                                                                                      376 ANGKPICSTGQFNXDVASMLNLYRASQLAFPGENILDEAKSPATKYLREALEKSETSSAW
                                                                                                                                                                                                                                                                                                           494 AVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKYLELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 AKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNTVNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674 GYDCLKEQCRDVLGYLRKVWEGLLASYTKRAEWSAKYVPTFNEYVENAKVSIALATVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 AWEAEKEÇGRELVSFFRKGWEDYLLGYYEEAEWLAAEYVPTLDEYIKNGITSIGQRILLL
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  LPYHLPFISQIHQKRQKXLQKIPLNVLHNHQTALLVSLEGLQDVVDWQBITNLQSRDGSF
                                                                              LSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734 NSI-PPTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grand fir; sesquiterpene synthase; disease resistance; fragrance; flavour.
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DGFGVSKLEVKDHIKECLIBPL 815
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gymnosperm; sesquiterpenoid;
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                                                                                                                                                    grand fir; sesquiterpene synthase; disease resistance; fragrance; flavour.
                                                                                                                                                                                                                                                                                                             끉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grand fir (Abies grandis) sesquiterpene synthase genes and protein products, useful for sesquiterpenoid production.
                                                                                                                                                                                                                                                                                       566. .570
/note= "conserved element, Asp residues function
coordination of a divalent cation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steele CL;
                                                                                                                B-alpha-bisabolene synthase computer-generated sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jetter R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON STATE RES FOUND.
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                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bohlman J,
AAY06567 standard; protein; 817
                                                                                                                                                    B-alpha-bisabolene synthase;
gymnosperm; sesquiterpenoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US001300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0072204P
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crock JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-458569/38.
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                                                                                                                                                                                                        Synthetic.
Abies grandis.
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574 GKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALATVVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (MATS/) MATSUDA S P
(SCHE/) SCHEPMANN H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-352584/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 817 AA;
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                                                                                                                                                                                                                                                                                                                                         Abies grandis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLDFNMVQALHQKETQHIVSWWRESGFNDLIFTRQRPVEMYFSVAVSMFEPEFAACRIAY 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSPASTACVFWHIQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 AVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKYLELA 553
                                                                                                                                                                                                                                                                                                                                                                                                       LPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGSF 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKSLGLD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the B-alpha-bisabolene synthase of grand fir (Abies grandis), a wound-inducible enzyme capable of generating multiple esquiterpenes, especially B-alpha-bisabolene, from farnesyl diphosphate. Another deduced sequence (see AAY06566) for the enzyme has Val at position 65. The invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives
                                                                                                                                                                                                                                                                                                                                                                            434 EKGDFFCFAGGTQIGYTDNINLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNAFDKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 AKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLXNTVNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                     Grand fir (Abies grandis) sesquiterpene synthase genes and protein products, useful for sesquiterpenoid production.
                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                    45.5%; Score 2114.5; DB 2; Length 817; 49.5%; Pred. No. 3e-182;
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 49.5%; Pred. No. 3e-182;
Matches 397; Conservative 159; Mismatches 227; Indels
                                                  Steele CL;
                                                    Bohlman J, Jetter R,
                              (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                       Claim 19; Page 71-74; 136pp; English.
           98US-0072204P
                                                     Crock JE,
                                                                        WPI; 1999-458569/38.
N-PSDB; AAX87504.
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New purified and isolated nucleic acid sequence encoding a
levopimaradiene synthase useful for producing pure ginkgolides in cells
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                                                                                                                             SGVLIMDGQLLSQEALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASSIECY
                                                                                         334 NSI-FFIGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida albicans; Kluyeromyces lactis; Saccharomyces; white fir; E-alpha-bisabolene synthase.
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Best Local Similarity 49.5%; Pred. No. 3e-182;
Matches 397; Conservative 159; Mismatches 227; Indele
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Crock JE,
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Misc-difference
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                                                                           21-JAN-1999;
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                                                                   SCVLVLLKWANVGDLQVEQGIEFIKSNLELVKDETDQDSLVTDFEIIFPSLLREAQSLRLG
                                                                                                                                ANGKFICSTGQFNKDVASMLNLYRASQLAFPGENILDEAKSFATKYLREALEKSETSSAW
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        T--NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVLNTL
                                                            ACLITIKIWNKGDIQVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKSLGLD
                                                                                        LPYHLPPISQIHQKRQKKIQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGSP
                                                                                                LSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY
                                                                                                                                                    PKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENFRD
                                                                                                                                                            EKGDPPCFAGQTQIGVTDNLNLYRCSQVCPPGEKIMEEAKTFTTNHLQNALAKNNAFDKW
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gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour.
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        | |: || || | : || || RRTANPHPNVWGYDLVHSLKSP-
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This sequence represents the B-alpha-bisabolene synthase of grand fir (Abies grandis), a wound-inducible enzyme capable of generating multiple sesquiterpenes, especially E-alpha-bisabolene, from farnesyl diphosphate. The sequence differs from the sequence of B-alpha bisavolene synthase AGI (see AAY06562) by a single residue, AGI having an Ala residue at position 55. The invention provides symnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a symnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives 136 256 316 136 194 253 196 313 373 375 433 493 9/ LSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY RLNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKRIQTLVKBIQCMFQS--MGDGB ACLLTLKIWNKGDIQVQKGVEFVRKHMBEMKDEAD-NHRPSGFEVVFPAMLDEAKSLGLD LPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGSF FKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENFRD **EKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNAFDKW** Gaps 'n Grand fir (Abies grandis) sesquiterpene synthase genes and protein products, useful for sesquiterpenoid production. residues function 19; 2; Length 817; ñ Indels Steele element, Asp red divalent cation 45.5%; Score 2113.5; DB 2; llarity 49.5%; Pred. No. 3.7e-182; Conservative 159; Mismatches 227; /note= "Ala in AG1 (AAY06563)" Bohlman J, Jetter R, FOUND Example 11; Page 92-95; 136pp; English. 566. .570 /note= "conserved coordination of a (UNIW) UNIV WASHINGTON STATE RES 99WO-US001300 98US-0072204P

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                                                                                                                                                          850
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                       495
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                                                                   AKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNTVNGF
                                                                           GKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALATVVL
                                                                                                                                                          MRENPECTEEEALSHVYGIIDNALKELAWFELANPASNAPLCVRRLLFNTARVMQLFYMYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the sequence of an E-alpha-bisabolene synthase polypeptide encoded by a computer-generated nucleic acid (see AAX87531) based on
       AVKKOLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKYLELA
                AWEAEKEGGRELVSFFRKGWEDYLLGYYEEAEWLAAEYVPTLDEYIKNGITSIGGRILLL
                                                                                                                              NSI-FFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCY
                                                                                                                                      SGVLIMDGQLLSQEALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASSIECY
                                                                                                                                                                                                                                                                                                      grand fir; sesquiterpene synthase; disease resistance; fragrance; flavour.
                                                                                                                                                                                                                                                                                                                                                           566. .570 // Anote= "conserved element, Asp residues function in coordination of a divalent cation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    grand fir (Abies grandis) sesquiterpene synthase genes and products, useful for sesquiterpenoid production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steele CL;
                                                                                                                                                                                                                                                                                         E-alpha-bisabolene synthase computer-generated sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jetter R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page 104-106; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RES FOUND
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bohlman J,
                                                                                                                                                                                          DGFGISDKEMKDHVSRTLFDPV 872
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                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US001300
                                                                                                                                                                                                                                                                                                         sbolene synthase;
sesquiterpenoid;
                                                                                                                                                                                                                                              AAY06568 standard; protein;
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crock JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-458569/38.
N-PSDB; AAX87531.
                                                                                                                                                                                                                                                                                                         E-alpha-bisabolene
                                                                                                                                                                                                                                                                                                                              Synthetic.
Abies grandis.
                                                                                                                                                                                                                                                                                                                                                                                          WO9937139-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-1998;
                                                                                                                                                                                                                                                                            08-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Croteau RB,
                                                                                                                                                                                                                                                                                                                 gymnosperm;
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                                                                                                                                                                                           851
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AAX87504). It contains conservative amino acid substitutions relative to the native sequence (see AAY0552). B-alpha-bisabolene synthase is a two mud-inducible enzyme capable of generating multiple sesquiterpenes, especially E-alpha-bisabolene, from farnesyl diphosphate. The invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                T--NESAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVLNTL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 EKGDFFCFAGOTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLONALAKNNAFDKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 AVKKDLPGEVEYALKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKYLELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFAACRIAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSI-FFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACLLTLKIWNKGDIQVQKGVEFVRKHMEBMKDFAD-NHRPSGFFVVFPAMLDFAKSLGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY
                                                                                                                                                                                                                                                                                                                                                                             RLNADYHPAVWKDDF1DSLTSPNSHATSKSSVDETINKRIQTLVKEIQCMFQS--MGDGE
                                                                                                                                                                                                                                                                                                                                                                                                LPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGSF
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                       Length 817;
                                                                                                                                                                                                                                                                                                     45.5%; Score 2113.5; DB 2; Length
llarity 49.5%; Pred. No. 3.7e-182;
Conservative 159; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 397; Conservat
                                                                                                                                                                                                                                                                          Sequence 817 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374
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DGFGISDKEMKDHVSRTLFDPV

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434 EKGDPFCFAGGTQIGVTDNIALYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNAFDKW 493
376 ANGKFICSTGQFNKDVASMIALYRASQLAFPGENILDEAKSFATKYLREALEKSETSSAW 435
                                                            256
                                                                                                                                                                                                                                                                                                                                                           556 TKVACLQIVLDDMYDIYGTLDELKLFTEAVRRWDLSFTENLPD-YMKLCYQIYYDIVHEV 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRENPECTEEBALSHVYGIIDNALKELNWELANPASNAPLCVRRLLFNTARVMQLFYMYR 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycrene synthase; limonene synthase; pinene synthase; flavour; monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
                                            :: |:|| ||:|| |::|| 675 SGVLIMDGQLLSQEALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASSIECY
                                                                                                                                                                                                     KLDFNNVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSWFEPEFAACRIAY
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                                                                                                   LSSPASTACVPMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY
                                                                                                                                                                            374 PKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENPRD
                                                                                                                                                                                                                                                                                                                                       494 AVKKOLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKYLELA
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                      LPYHLPPISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQBITNLQSRDGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALATVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grand Fir monoterpene synthase clone AG1.28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGFGISDKEMKDHVSRTLPDPV 872
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DGFGVSKLEVKDHIKECLIEPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abies grandis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes the heterologous expression of taxane analogues, comprising a DNA sequence comprising a taxane synthesis pathway, making a DNA construct in which the DNA sequence is under control of regulatory elements, introducing the DNA construct into a host cell, growing the host cell to produce taxane analogues, and recovering the required taxane from the culture medium. Also described: (1) an isolated DNA sequence comprising the taxane synthesis pathway, the isolated DNA sequence comprising the taxane synthesis pathway expression vector comprising the isolated DNA sequence; and (3) a host cell comprising a taxane synthesis pathway derived from a taxane-producing organism, plant or tree, the taxane synthesis pathway is foreign to the host cell. The axane analogues have cytostatic activity, and so can be used as anticancer agents. The present sequence represents a taxadiene synthase homologous protein, which is given in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T--NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVLNTL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKSLGLD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |: || || || : || || || STANPHPNVWGYDLVHSLKSP-----YIDSSYRERAEVLVSEIKVMLNPAITGDGE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heterologous production of taxane analogs related compound useful as anticancer agent involves cloning a full-length taxane synthesis pathway from a taxan-producing organism into a taxane-resistant host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 RLNADYHPAVWKDDPIDSLTSPNSHATSKSSVDETINKRIQTLVKEIQCMFQS---MGDGE
                                                                                                                                                                                                                                                                              Faxane, taxane synthesis; taxadiene synthase; cytostatic; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.5%; Score 2113.5; DB 5; Length larity 49.5%; Pred. No. 3.7e-182; Conservative 159; Mismatches 227; Indels
                                                                                                                                                                                                                                       Taxadiene synthase homologous protein sequence y06566.
|||||:| |:|||:
DGFGVSKLEVKOHIKECLIEPL 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 1; 60pp; English.
                                                                                                                     ABB79391 standard; protein; 817
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29-NOV-2000; 2000US-0253843P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2001; 2001WO-DK000763
                                                                                                                                                                                                   (first entry)
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397; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           WO200240694-A2
                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                               13-AUG-2002
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Best Local Si
Matches 397,
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                      794
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Sequence 782 AA;
  N-PSDB; AAX08654
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Nucleotide sequences encoding mycrene synthase, limonene synthase and pincaputhase from Grand fir may be incorporated into any organism (e.g. intact plant, animal, microbe), or derived cell culture that produces geranyl diphosphate for the production of the aforementioned calls may also be used for the production of the aforementioned cancer properties, improvement of defense capability, and the alteration of that derivatives. In particular they can be used for the production of other ecological interactions mediated by mycrene, limonene, pinene, or their derivatives. In particular they can be used for the production of plant seeds for the extraction of oil or meal. cDNAs encoding myrcene synthase, pinene synthase and limonene synthase from Grand Fir were solated and sequenced by the following procedure. Based on comparison of sequences of different plant synthase enzymes, four conserved sequences capability and the other three sense primers of the construction of four degenerate primers (AAXO8646 and AAXO8645 generated a PCR product which was 110 base pairs in compath. The amplified product was used in a plasmid construct to transform E.coli XLI-Blue cells and the inserts were sequenced. Four probes (AAXO8650-53) were devised from the sequenced insert and were used to screen a Grand Fit cDNA library. One of these clones identified are synthase sequence given in AAXO8649. The other clones identified are synthase sequence given in AAXO8649. The other clones identified are
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New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 DFIDSLISPNSHATSKSSVDETINKRIQTLVKEIQCMFQS--MGDGET--NPSAYDTAWV
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44.9%; Score 2085.5; DB 2; Length
Best Local Similarity 49.6%; Pred. No. 1.2e-179;
Matches 391; Conservative 158; Mismatches 221; Indels
                                                                                                                                               Example 1; Page 90-92; 121pp; English.
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The present invention describes an isolated terpene synthase (I) comprising a region with at least 20% identity to region 265-535 of a 548 amino acid (as) sequence (Ia), given in AAY90831. (I) contains nine alpha carbon atoms (alphaC) that have interatomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthase; protein co-ordinate data; active site; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; plyment; antitumour; steroid hormone; signal transduction pathway; blia caid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           producing terpene
agents, are derived from known
                                                                                                                                                                                               863
                                                                                                                                           803
                                                                                                                                                                                                                      771
SFFRKGWEDYLLGYYEEAEWLAAEYVPTLDEYIKNGITSIGGRILLLSGVLIMDGQLLSQ
                                                                                                                                           746 YILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCYMRENPECTEEEAL
                                                                                                                                                         804 SHVYGIIDNALKELNWELANPASNAPLCVRRLLFRNTARVMQLFYMYRDGFGISDKEMKDH
                                                                                                                                                                                                             YDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDVL
                                                     Grand fir E-alpha-bisabolene synthase protein sequence SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chappell J, Manna KR, Noel JP, Starks CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel terpene synthase enzymes, useful for hydrocarbons, e.g. fragrances or antitumor enzymes by specific amino acid alterations.
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                                                                                                                                                                                                                                                                                                                                            AAY90853 standard; protein; 782 AA.
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99US-0130628P.
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772 IKECLIEPL 780
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Steele CL, Bohlmann J,
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772 IKECLIEPL
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Matches
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                 arrangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (1), and related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precursors of steroid hormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids corocidity then) are used as controls in the analysis of products formed by encoding then) are used as controls in the analysis of products formed by corymatic synthesis; as nutrient supplements; for affinity purification of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthase may produce novel terpene products. AAA38910 to AAA38938 and AAY30831 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38935 represent invention
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The present invention describes the heterologous expression of taxane analogues, comprising cloning a DNA sequence comprising a taxane synthesis pathway, making a DNA construct in which the DNA sequence is under control of regulatory elements, introducing the DNA sequence is a host cell, growing the host cell to produce taxane analogues, and recovering the required taxane from the culture medium. Also described: (1) an isolated DNA sequence comprising the taxane synthesis pathway); (2) an isolated DNA sequence; and (3) a host cell comprising the isolated DNA sequence; and (3) a host cell comprising a taxane synthesis pathway derived from a taxane-producing organism, plant or tree, the taxane synthesis pathway is foreign to the host cell. The taxane analogues have cytostatic activity, and so can be used as homologous protein, which is given in an example from the present
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       aB
Heterologous production of taxane analogs related compound useful anticancer agent involves cloning a full-length taxane synthesis ffrom a taxan-producing organism into a taxane-resistant host cell.
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                                                                                                      Example 3; Fig 1; 60pp; English
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DELVVKIKDMFNALGDGDISPSAYDTAWVARLATISSDGSEKPRFPQALNWVFNNQLQDG 176
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                                                        This is a cloned pacific yew taxadiene synthase (TS) protein. The sequence can be used to increase to increase taxol biosynthesis into taxoids in transformed cells. The protein can be modified to improved efficiency, and to redirect the targeting of the expressed polypoptide. The modifications can be to alter catalytic efficiency, to modify substrate utilisation, and to alter product outcome. The antibodies specific for the mature native pacific yew TS polypeptide can be used to purify TS polypeptides, cloning TS homologues from Pacific yew or other plant species, and as probes for blots and immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 KMNALGNKAIHDPTNCRAKSERQMMWVCSRSGRTRVKMSRGSGGPGPVVMMSSSTGTSKV 70
                                                                                                                                                                                                                                                                                              taxadiene synthase; taxol biosynthesis; probe; immunoassay.
AAETRP---DQLPQEERFVSRLNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKRI
                                         SHVYGIIDNALKELNWELANPASNAPLCVRRLLFNTARVMQLFYMYRDGFGISDKEMKDH
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biosynthesis.
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                                                                     SLEGLQDVVDWQEITINLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPC
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SWGBECTFLAYDRVLNTLACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSGF
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                                            LCVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPV 872
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61.2%; Score 2844; DB 4; Length 8
Best Local Similarity 62.3%; Pred. No. 2.7e-279;
Matches 546; Conservative 120; Mismatches 183; Indels
                    US-08-405-254-6
US-08-326-286-4
US-08-326-286-4
US-08-21-465-1
US-09-86-171-48
US-09-234-393-44
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US-09-907-072-48
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Patent No. 646872
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TILE REFERENCE: 07678-025001
CURRENT APPLICATION UNMBER: 05/00,993
FILE REFERENCE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-08-22
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FRAELSEQ for Windows Version 3.0
SEQ ID NO 56
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TYPE: PRT; ORGANISM: Abies grandis
US-09-398-395A-56
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/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
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                         GenCore version 5.1.6
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gequence 56, Application US/09895752
Patent No. 6559297
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 65592971, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: STARKS, COURTNEY M.
APPLICANT: STARKS, COURTNEY M.
APPLICANT: STARKS, COURTNEY M.
APPLICANT: STARKS, COURTNEY M.
APPLICANT: STARKS, COURTNEY M.
APPLICANT STARKS, STARTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/895,752
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Best Local Similarity 62.3%; Pred. No. 2.7e-279;
Matches 546; Conservative 120; Mismatches 183; Indels 2
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US-09-887-586A-56

Sequence 56, Application US/09887586A

Batent No. 6495354

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Rarks, Coutrey M.
APPLICANT: Barks, Coutrey M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-06-12
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 58

SOFTWARKE: PASSEE FOR WINDOWS VERSION 3.0

SOFTWARKE: 9885EQ for Windows Version 3.0

SENGTH: 868
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ORGANISM: Abies grandis
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           SAAETRPDQLPQEERFVSR---LNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKR
                                                                                          WGEECI FLAYDRVLNTLACLLTLKI WNKGDI QYQKGVE FVRKHMEEMKDEADNHR PSGFE
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TYPE: PRT
ORGANISM: Abies grandis
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR PILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Abies grandis
US-09-895-752-56
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                   63 GGATSVPYQSAEKNDSLSSSTLVKREFPPGFWKDDLIDSLTS--SHKVAAS--DE---KR
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RNRGELVSSVOCYMRENPECTEERALSHVYGI I DNALKELNWELANPASNAPLCVRRLLF
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                                                                                                     873
                                                                              NTARVMQLFYMYRDGFGIS-DKEMKDHVSRTLFDPVA
                                                                                                                                                                                                                                                                            APPLICANT: Chappell, Joseph
APPLICANT: No. 65696561, Joseph
APPLICANT: Searks, Coutrney M.
APPLICANT: Searks, Coutrney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012B
CURRENT FILING DATE: 1998-00-18
FRIOR APPLICATION NUMBER: 60/100,993
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR PILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FRASEQ for Windows Version 3.0
SEQ ID NO 56
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Sequence 13, Application US/09234393A
; Sequence 13, Application US/09234393A
; Patent No. 6265639
; GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
; APPLICANT: Croteau, Rodney B
; APPLICANT: Croteau, Rodne B
; APPLICANT: Steele, Christopher L
; APPLICANT: Steele, Christopher L
; TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: WSUR113345
; TITLE OF INVENTION UNMBER: US/09/234,393A
; CURRENT FILING DATE: 1999-01-20
; BARLIER APPLICATION NUMBER: 60/072,204
; BARLIER APPLICATION NUMBER: 60/072,204
; BARLIER PATENT OF SEQ ID NOS: 55
; SOFTWARE: PATENTIN Ver. 2.0
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176 WGEGFYFLAYDRILATLACIITLTLWRTGBTQVQKGIEFFRTQAGKWEDEADSHRPSGFE 235
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                                                          RIMAVDTVERLGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILR
                                       VVFPAMLDEAKSLGLDLPYHLPFISQIHQKROKKLOKIPLNVLHNHQTALLYSLEGLQDV
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                                                                      VYKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRORPVEMYFSV 597
             YVENAKVSIALATVVILNSI FFTGELLPDYILQQVDLRSKFLHLVSLTGRLINDTKTYQAE
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Best Local Similarity 62.3%; Pred. No. 2.7e-279;
Matches 546; Conservative 120; Mismatches 183; Indels 2
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APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02500, 797
CURRENT PILING DATE: 2001-07-06
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
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US-09-900-797-56
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                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: protein
PEATURE:
NAME/KEY:
MANE/KEY:
LOCATION: (1)...(817)
OTHER INFORMATION: Computer-generated protein sequence
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                        , OTHER INFORM
US-09-234-393-40
                                                                                                                                               LENGTH: 817
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APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, John B
APPLICANT: Bohlman, Jorg
APPLICANT: Steele, Christopher L
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    Pred. No. 3.3e-205;
); Mismatches 227; Indels
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US-09-234-393-40
'S Equence 40, Application US/09234393A
'Patent No. 6265639
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DGFGVSKLEVKDHIKECLIEPL
  Similarity 49.5%; Pr
97; Conservative 159;
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GENERAL INFORMATION:
APPLICANT: Crock, John E
APPLICANT: Crock, John E
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES |
TITLE OF INVENTION: AND METHODS OF USE
TITLE REPERENCE: WSUR11746
CURRENT APPLICATION NUMBER: 09/244,393
PRIOR APPLICATION NUMBER: 09/244,393
PRIOR APPLICATION NUMBER: 60/072,204
PRIOR PILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 40
LENGTH: 817
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794 DGFGVSKLEVKDHIKECLIEPL 815
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                                                                                                                                                                                                          Sequence 13, Application US/09865171

Sequence 13, Application US/09865171

Sequence 11, Application US/09865171

Septent No. 6451576

GENERAL INFORMATION:

APPLICANT: Crockau, Rodney B

APPLICANT: Steele, Christopher L

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: AND METHODS OF USE

TITLE OF INVENTION: AND METHODS OF USE

TITLE REPRESENCE: WORML17468

CURRENT FILING DATE: 2001-05-24

FRIOR FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-20

SOFTWARE: PARCAIL USE: 1999-01-20

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                 735 MKDHPECTEEEALDHIYSILEPAVKELTREFLKP-DDVPFACKKMLFEETRVTMVIFKDG 793
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Best Local Similarity 49.5%; Pred. No. 3.3e-205;
Matches 397; Conservative 159; Mismatches 227; Indels
                                                                      DGFGISDKEMKDHVSRTLFDPV 872
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DGFGVSKLEVKDHIKECLIEPL 815
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US-09-865-171-13
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                                                                                                                                                                          SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
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                                                          674 GKDGLKEÇGRDVLGYLRKVWEGLLASYTKEAEWSAAKXVPTFNEYVENAKVSIALATVVL
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Best Local Similarity 49.5%; Score 2114.5; DB 4; Length 817;
Best Local Similarity 49.5%; Pred. No. 3.3e-205;
Matches 397; Conservative 159; Mismatches 227; Indels 19;
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OTHER INFORMATION: protein
NAME/KEY: misc_feature
LOCATION: (1)..(817)
COLATION: (1)..(817)
OTHER INFORMATION: Computer-generated protein sequence
US-09-865-171-40
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                                                                                  FKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENPRD
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              T -- NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVLNTL
                         SMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIQSHPLLSDRLLATL
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Fatent No. 6265639
GENERAL INFORMATION:
APPLICANT: Crock, John E
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
TITLE REPERENCE: WSUR113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER RPLICATION NUMBER: 60/072,204
SARLIER PILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
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US-09-234-393-42
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             ANGKFICSTGQPNKDVASMLNLYRASQLAFPGENILDEAKSFATKYLREALEKSETSSAW 435
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LSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRY
                                                       PKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENFRD
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APPLICANT: Croteau, Rodney B
APPLICANT: Crotex, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRAN)
TITLE OF INVENTION: MURBER: US/09/234,393A
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER PILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6265639
GENERAL INFORMATION:
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US-09-234-393-38
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US-09-234-393-38
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; TYPE: PRT
; ORGANISM: Ables grandis
US-09-865-171-38
      RESULT 12
US-09-865-171-38
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                                                                                                                                         Gapa
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                                                                                                                      DB 3; Length 817;
                                                                                                                     Query Match
Best Local Similarity 49.5%; Pred. No. 4.2e-205;
Matches 397; Conservative 159; Mismatches 227; Indels
                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(817)
OTHER INFORMATION: Computer-generated protein sequence
US-09-234-393-42
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DGFGVSKLEVKDHIKECLIEPL 815
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                  TYPE: PRT ORGANISM: Artificial Sequence
SEQ ID NO 42
LENGTH: 817
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                                                                                                                                     SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
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45.5%; Score 2113.5; DB 4; Length
Best Local Similarity 49.5%; Pred. No. 4.2e-205;
Matches 397; Conservative 159; Mismatches 227; Indels
US-09-865-171-3

US-09-865-171-3

Patent No. 6451576

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Crock, John E

APPLICANT: Bohlmann, Orga

APPLICANT: Steele, Christopher L

TITLE OF INVENTION: SEGUITERPENE SYNTHASES I

TITLE OF INVENTION: AND METHODS OF USE

TITLE OF INVENTION: NAUMER: US/09/865,171

CURRENT FILING DATE: 2001-05-24

PRIOR FILING DATE: 1999-01-20

PRIOR FILING DATE: 1999-01-22

NUMBER OF SEQ ID NOS: 55

SOFTWARR: Patentin Ver. 2.0

SEQ ID NO 38

LENGTH: 817
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Sequence 16, Application US/09360545

Fatent No. 6429014

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Steele, Christopher L

APPLICANT: Phillips, Michael A

TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

FILE REFERENCE: wauri3885

CURRENT APPLICATION NUMBER: US/09/360,545

CURRENT PILING DATE: 1999-07-26

EARLIER APPLICATION NUMBER: PCT/US98/14528

EARLIER FILING DATE: 1997-11-07

EARLIER FILING DATE: 1998-07-10

NUMBER OF SEQ ID NOS: 107
                                                       208 IQVQKGVEFVRKHMBEMKDEAD-NHRPSGFEVVFPAMLDEAKSLGLDLPYHLPFISQIHQ 266
                                                                                                                                                                                         KLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFAACRIAY 613
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317 FEKEIKEALDYVYRHWN-ERGIGWGRLNPIADLETTALGFRLLRLHRYNVSPAIFDNFKD 375
                                     134 EKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNAFDKW 493
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44.9%; Score 2085.5; DB 4; Length
Best Local Similarity 49.6%; Pred. No. 2.7e-202;
Matches 391; Conservative 158; Mismatches 221; Indels
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; ORGANISM: Abies grandis
US-09-360-545-16
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US-09-360-545-16
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APPLICANT: Croceau, Rodney B
APPLICANT: Crock, John B
APPLICANT: Bohlmann; Jornal B
APPLICANT: Scele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/865,171
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/234,393
PRIOR PILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-22
AWEAEKEQGRELVSFFRKGWEDYLLGYYEEAEWLAAEYVPTLDEYIKNGITSIGQRILLL 674
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                                                         SGVLIMDGQLLSQEALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASSIECY
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                                                                                                                                                                                         DGFGISDKEMKDHVSRTLFDPV 872
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DGFGVSKLEVKDHIKECLIEPL 815
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US-09-865-171-42
; Sequence 42, Application US/09865171
; Patent No. 6451576
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 817
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Query Match
44.9%; Score 2085.5; DB 4; Length
Best Local Similarity 49.6%; Pred. No. 2.7e-202;
Matches 391; Conservative 158; Mismatches 221; Indels
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 RYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENFRDEKGDFFCFAGOTO
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                                            687 GYLRKVWEGILLASYTKEAEWSAAKYVPTFNEYVENAKVSIALATVVLNSI-FFTGELLPD
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Search completed: August 17, 2004, 21:03:48
Job time : 21.8728 secs
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Sequence 46, Application US/09398395A
Sequence 46, Application US/09398395A
Patent No. 6468772.
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHARES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: 06/093
FILE REFERENCE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-06-13
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NUMBER: 60/150,262
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE FASTESQ for Windows Version 3.0
SEQ ID NO 46
ILENGTH: 782
TYPE: PRI
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447 IGVIDNIALYRCSQVCFPGEKIMEEAKTFTINHLQNALAKNNAFDKWAVKKDLPGEVEYA

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ETQHIVSWWRESGFNDLTFTRORPVEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDL 626

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Sequence 46, Appl Sequence 16, Appl Sequence 14, Appl Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl Sequence 386, Appl Sequence 88, Appl Sequence 182585, Sequence 182585, Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 18, Appl Sequence 58, Appl Sequence 24, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mart, Seitchi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: PO20a0US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 358
LENGTH: 873
0 US-09-900-797-46

2 US-09-893-820-46

3 US-10-041-007-16

4 US-10-025-145A-16

1 US-09-903-012-44

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 873; Conservative 0; Mismatches
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Publication No. US20040072323A1
GENERAL INFORMATION:
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Sequence 2, Appli
                                                                                                August 17, 2004, 21:02:37; Search time 47.4515 Seconds (without alignments) 5775.546 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-007-3
US-10-041-007-35
US-10-041-007-35
US-10-041-007-39
US-09-903-012-56
US-09-903-012-56
US-09-903-012-56
US-09-903-013-88
US-10-041-018-388
US-10-041-018-388
US-10-041-018-388
US-10-041-018-388
US-10-041-007-4
US-10-041-007-4
US-10-903-012-46
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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and is derived by analysis of
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seq length: 200000000
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Sequence:

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                                       MAGVLFANLPCSLQLSPKVPFRQSTNILIPFHKRSSFGFNAQHCVRSHLRLRWNCVGIHA
          Levopimaradiene Synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/10041007; Sequence 33, Application No. US20020164736A1; GENERAL INFORMATION:
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Schepmann, Hala G; TITLE OF INVENTION: Ginkgo Biloba Levopimara; FILE REFERENCE: PO2081US1; CURRENT APPLICATION NUMBER: US/10/041,007; PRIOR APPLICATION NUMBER: US/202-01-07; PRIOR APPLICATION NUMBER: US/2059,881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-041-007-33
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; GENERAL INFORMATION:
; APPLICANT: Matsuda, Salichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase; PILE REFERRNCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; RIOR PILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 2.
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100.0%; Pred. No. 0;
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; ORGANISM: Ginkgo biloba
US-10-041-007-2
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PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 873
                                                 ; TYPE: PRT
; ORGANISM: Ginkgo biloba
US-10-041-007-33
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Sequence 35, Application US/10041007
; Sequence 35, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Selichi P.T.
; APPLICANT: Schepmann, Hala G
; TILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US 60/259,881
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; NUMBER OF SEQ ID NOS: 41
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93.0%; Score 4319; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 813; Conservative 0; Mismatches
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US-10-041-007-35
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860 MXDHVSRTLFDPVA 873
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ORGANISM: Ginkgo biloba
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US-10-041-007-39
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                                                                                             Sequence 37, Application US/10041007

Dublication No. US20020164736A1

GENERAL INFORMATION:
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase;
FILE REFERENCE: P02081US1

CURRENT APPLICATION NUMBER: US/10/041,007

CURRENT FILING DATE: 2002-01-07

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.1
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                                   RVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 873
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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Matches 794; Conservative
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US-10-041-007-37
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                                                                                                           GEILPDYILQQVDLRSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCYMRENPECTE
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                                     BQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSTALATVVLNSIFFT
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Sequence 39, Application US/10041007

Publication No. US20020164736A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Mateuda, Selichi P.T.

APPLICANT: Schepman, Hala G

TITLE OF INVENTION: Glinky Biloba Levopimaradiene Synthase

FILE REFERENCE: PO2081US1

CURRENT FILICATION NUMBER: US/10/041,007

FRIOR APPLICATION NUMBER: US 60/259,881

PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR PILICATION NUMBER: US 60/259,881

PRIOR PRILICATION NUMBER: US 60/259,881

FRIOR PRILICATION NUMBER: US 60/259,881

SOFTWARE: Patentin version 3.1

SEQ ID NO 39

LENGTH: 746
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches
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 236 IVPPAMLKEAKILGLDLPYDLPFLKQIIEKREAKLKRIPTDVLYALPTTLLYSLEGLQBI
                                     298 VDWQEITWLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFE
                                                                                                             RLWAVDTVERLGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILR
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APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012
CURRENT FILING DATE: 2001-07-11
PRIOR FILING DATE: 1999-09-17
PRIOR PELING DATE: 1999-09-17
PRIOR PELING DATE: 1999-04-22
PRIOR PELING DATE: 1999-04-22
PRIOR PELING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
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US-09-903-012-56
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Best Local Similarity 62.3%; Pred. No. 5.9e-262;
Matches 546; Conservative 120; Mismatches 183;
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Sequence 56, Application US/09887586A

Patent No. US20020094556A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094556A11, Joseph
APPLICANT: Roarks, Courtney M.
APPLICANT: Rana, Kathleen R.
ITLE OF INVENTION: SYNTHASES
FILE REFERENCE: O7678-025011
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 00/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 56
LENGTH: 868
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                            63 GGATSVPYQSAEKNDSLSSSTLVKREFPPGFWKDDLIDSLTS--SHKVAAS--DE---KR
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); Mismatches 183;
al Similarity 62.3%; Pr 546; Conservative 120;
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Best Local Similarity 62.3%; Pred. No. 5.9e-262;
Matches 546; Conservative 120; Mismatches 183;
TITLE OF INVENTION: SYNTHABES
FILE REFERENCE: 07678-02501,
CURRENT APPLICATION NUMBER: US/09/900,797.
CURRENT FILING DATE: 2001.07-06
FRIOR FILING DATE: 1999-017
FRIOR FILING DATE: 1999-04-22
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CORGANISM: Abies grandis
US-09-900-797-56
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NS-09-900-797-56
Sequence 56, Application US/09900797
Publication No. US20030087406A1
GENERAL INFORWATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20030087406A11, Joseph
APPLICANT: Starke, Courtney M.
RAPLICANT: Manna, Kathleen R.

537 534

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238 VVFPAMLDEAKSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDV 297
415 LHGYNVSSDVLKTFRDENGEPFCFLGQTQRGVTDMLNVNRCSHVSFPGETIMEEAKLCTE 474
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; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Mateuda, Selichi P.T.
; APPLICANT: Mateuda, Selichi P.T.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REPRENENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR PILING DATE: 2001-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; NUMBER OF SEQ 1D NOS: 413
; SOFTWARE: Patentin version 3.1
; SOFTWARE: Patentin version 3.1
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US-10-041-018-388
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                837
                                   SAAETRPDQLPQEERFVSR---LNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKR 117
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                                                                                    NTARVMQLFYMYRDGFGIS-DKEMKDHVSRTLFDPVA 873
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Best Local Similarity 62.3%; Pred. No. 5.9e-262;
Matches 546; Conservative 120; Mismatches 183;
                                                                                                                                                                                                                                                                           APPLICANT: No. US20040053386A11, Joseph P. APPLICANT: Starks, Courtney M. APPLICANT: Starks, Courtney M. APPLICANT: Manna, Kathleen R. TITLE OF INVENTION: SYNTHASES FILE REFERENCE: 07678-025001 CURRENT APPLICATION NUMBER: US/09/893,820 CURRENT FILING DATE: 1999-09-17 PRIOR FILING DATE: 1999-09-17 PRIOR FILING DATE: 1999-09-17 PRIOR PLICATION NUMBER: 60/130,628 PRIOR FILING DATE: 1999-09-18 PRIOR PLILING DATE: 1999-09-18 PRIOR APPLICATION NUMBER: 60/130,628 PRIOR FILING DATE: 1999-04-22 PRIOR APPLICATION NUMBER: 60/130,628 PRIOR FILING DATE: 1999-04-22 PRIOR FILING DATE: 1999-04-22 PRIOR FILING DATE: 1999-08-23 NUMBER OF SEQ ID NOS: 58 COTTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                          Sequence 56, Application US/09893820 Publication No. US20040053386A1 GENERAL INFORMATION: APPLICANT: Chappell, Joseph
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; ORGANISM: Abies grandis
US-09-893-820-56
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61 SAAETRPDOLPQEERFVSR---LNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKR
                118 IQTLVKEIQCMFQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGS
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APPLICANT: Schepman, Hala G
TITLE OF INVENTION: Glange Biloba Levopimaradiene Synthase
TITLE REPERRACE: P02081USI
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT PILING DATE: 2002-01-07
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
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US-10-041-007-15
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Sequence 4, Application US/10041007

Publication No. US2002016473641

GENERAL INFORMATION:

APPLICANT: Matesuda, Seiichi P.T.

APPLICANT: Schepmann, Hala G

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

FILE REFERENCE: PO2081US1

CURRENT APPLICATION NUMBER: US/10/041,007

CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Version 3.1

SEQ ID NO 4
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Best Local Similarity 62.3%; Pred. No. 5.9e-262;
Matches 546; Conservative 120; Mismatches 183;
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ORGANISM: Abies grandis
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                                                              Gaps
                                          45.5%; Score 2114.5; DB 13; Length 817;
larity 49.5%; Pred. No. 2.9e-192;
Conservative 159; Mismatches 227; Indels 19;
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DGFGVSKLEVKDHIKECLIEPL 815
                ; ORGANISM: Abies grandis
US-10-041-007-15
                                          Query Match
Best Local Similarity
Matches 397; Conserv
LENGTH: 817
TYPE: PRT
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RESULT 14
US-09-887-586A-46
; Sequence 46, Application US/09887586A
; Patent No. US20020094556A1
; Patent No. US20020094556A1
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.

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44.9%; Score 2085.5; DB 9;
Best Local Similarity 49.6%; Pred. No. 1.6e-189;
Matches 391; Conservative 158; Mismatches 221;
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REPERENCE: 07678-025001
CURRENT FILING DATE: 2001-06-22
FRIOR APPLICATION NUMBER: 09/398,395
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
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FRIOR APPLICATION NUMBER: 60/150,628
FRIOR APPLICATION NUMBER: 60/150,628
FRIOR APPLICATION NUMBER: 60/150,628
FRIOR FILING DATE: 1999-08-23
NUMBER: OF SEQ ID NOS: 58
SEQ ID NO 46
SEQ ID NO 46
LENCTH: 782
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US-09-887-586A-46
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44.9%; Score 2085.5; DB 9; Length 782;
Best Local Similarity 49.6%; Pred. No. 1.6e-189;
Matches 391; Conservative 158; Mismatches 221; Indels 19;
                                                          TYPE: PRT
ORGANISM: Abies grandis
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ETQHIVSWWRESGFNDLTFTRORPVEMYFSVAVSMFEBFRACRIAYAKTSCLAVILDDL | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                 YDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDVL
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Job time : 50.4515 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 VSRTLFDPV 872
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772 IKECLIEPL 780
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2004, 20:57:35; Search time 17.2551 Seconds

(without alignments)

4866.690 Million cell updates/sec
```

Title: US-10-041-007-2
Perfect score: 4645
Sequence: 1 MAGVLFANLPCSLQLSPKVP.......GISDKEMKDHVSRTLFDPVA 873
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		ent-kaurene synthe	kaurene synthase A	ent-kaurene syntha		ent-kaurene syntha	hypothetical prote	hypothetical prote	dien	limonene cyclase -	probable limonene	probable limonene	(+)-delta-cadinene	(+)-delta-cadinene	5-epi-aristolochen	sesquiterpene cycl	probable limonene	germacrene C synth	υ	hypothetical prote	hypothetical prote	vetispiradiene syn	probable terpene s	hypothetical prote	_	_		hypothetical prote	hypothetical prote	probable vetispira
SU		D85035	T02959	T06783	T09672	T52059	G96825	A96637	A56118	A48863	F71434	G71434	568365	868366	T03714	T08174	H84633	T06266	T06265	B96723	H86460	C56118	G86443	T05328	C71424	G96588	T06285	C96642	T05329	T00509
DB	1	2	~	7	~	~	~	~	~	~	~	~	~	~	~	N	N	N	N	~	~	~	~	7	7	~	~	7	~	7
% Query Match Length		802	823	801	789	785	785	870	520	599	900	1024	554	554	550	559	591	548	548	632	598	350	608	573	582	530	535	421	598	598
* Query Match		28.7	28.4	28.1	23.1	22.3	22.2	15.2	14.3	14.2	14.1	14.0	13.9	13.9	13.6	13.6	13.6	12.2	12.0	10.1	•	9.6	9.5	9.0	8.7	8.5	8.4	8.4	8.1	8.1
Score		1332	1318	1303	1072.5	1034	1033	705	663	099	654.5	650.5	647.5	643.5	•	633.5	633	565	559	469.5	460.5	448	443	416.5	403.5	393	389.5	388.5	375	374
Result No.	1 1	-	7	m	4	S	9	7	æ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

8 8 8 8

541 MLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVS 600

. probable cyclase -	probable terpene s	vetispiradiene syn	hypothetical prote	hypothetical prote	hypothetical prote	ent-kaurene syntha	ent-kaurene syntha	y4kT protein - Rhi	hypothetical prote	probable terpene c	5-epi-aristolochen	clostripain-relate	hypothetical prote	protein C44E4.1a [acetyl-CoA carboxy
H70972	F96684	B56118	T05331	T06287	D71424	JC7227	T00024	T10874	I40214	H96525	T03982	E72236	T30951	D87757	A29924
~	~	~	~	~	~	~	~	N	~	~	~	~	~	~	-
501	598	300	612	471	383	952	946	516	516	203	148	979	1131	3864	2324
8.0	7.9	7.6	7.5	7.1	6.7	ъ. В	5.4	4.9	4.4	3.6	3.3	3.1	5.9	5.9	2.8
371	369	351.5	349.5	330.5	313	271	250	227.5	203.5	166	151.5	146	135.5	135.5	132
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 D85035 ent-kaurene synthetase C;Species: Arabidopsis C;Date: 16-Feb-2001 #se C;Accession: D85035 R;anonymous, The Europe Nature 402, 769-777, 19 A;Hitle: Sequence and a A;Reference number: A85 A;Accession: D85035 A;Actus: preliminary A;Molecule type: DNA A;Residues: 1-802 <gto>A;Cesetios: C;Genetios: C;Genetios: A;Gene: A14902780 A;Map position: 4</gto>	RESULT 1 D85035 ent-kaurene synthetase A-like protein [imported] - Arabidopsis thaliana cippecies Arabidopsis Laliana (mouse-ear cress) C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C.Accession: D85035 C.Accession: D85035 C.Accession: D85035 A:Accession:
Query Match Best Local Matches 28	Ouery Match Best Local Similarity 36.6%; Pred. No. 2e-83; Matches 283; Conservative 146; Mismatches 254; Indels 90; Gaps 17;
Qy 12	122 VKEIQCMFQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGBE 181
6 90	8 VKSVKTILRNLTDGEITISAYDTAWVALIDAGDKTPAPPSAVKWIAENQLSDGSWGDA 155
Qy 18	182 CIFLAXDRVLNTLACLILTLKIWNKGDIQVQKGVFFVRKHMEBMKDBADNHRPSGFBVVFP 241
Db 15	6 YLFSYHDRLINTLACVVALRSWNLFPHQCNKGITFFRENIGKLEDENDEHMPIGFEVAFP 215
Qy 24	242 AMLDBAKSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLBGLQDVVDWQ 301
Db 21	6 SILETARGINIDVPYDSPVLKDIYAKKELKLTRIPKBIMHKIPTTLLHSLEGMRD-LDWE 274
Oy 30	302 EITNIQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWA 361
Db 27	S KLLKLÓSÓDGSFLFSPSSTAFAFMOTRDSNCLEYLRNAVKRFNGGVÞNVFPVDLFEHIMI 334
Qy 36	362 UDTVERLGIDRYFKKBIKESLDYVYRYMDAERGVGWARCNPIPDVDDTAMGLRILRLHGY 421
Db 33	:: :
Qy 42	422 NVSSDVLENFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQ 481
Db 39	4 QVSADVFKNF-EKEGEFFCFVGQSNQAVTGMFNLYRASQLAFPREEILKNAKEFSYNYLL 452

Db 385 AFRLIALHGYNVSPSVENF-EKDGEFFCFVGGSTQATGAYNLARASQISFQGEDVLHR 443 Qy 472 AKTFTTHHLQUALAKUNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEGF-GSN 530 444 ARVFSYEPLRQREEGGMIRDKWIVAKDLPGEVGYAIKYPWHRSMPRLEARSYIEGF-GSN 533 444 ARVFSYEPLRQREEGGMIRDKWIVAKDLPGEVGYTLDFPWYASLPRVEARTYLDGYGGKD 503 444 ARVFSYEPLRQREEGGMIRDKWIVAKDLPGEVGYTLDFPWYASLPRVEARTYLDGYGGKD 503 Qy 531 DVWLGKTLYRMPLUNNDTYLELARLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRRRP 590 QV 591 VENYFSYAVSMFEPEFAAGRIAYARTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISV 650 S61 LDSVRDNGLK	Db 704 LVQVIEICAGRIGEAVSMINNKONDWPIQLTCATCDSINHRMLLS 748 Qy 811 DNALKELA	Plant J. 11, 443-454, 1997 AjTile: The LS locus of pea encodes the gibberellin biosynthesis enzyme ent-kaurene sy. AjTile: The LS locus of pea encodes the gibberellin biosynthesis enzyme ent-kaurene AjReference number: 215810; MUID:97260958; PMID:9107034 AjReference number: 215810; MUID:97260958; PMID:9107034 AjResidues: Preliminary; translated from GB/EMBL/DDBJ AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 cALT> AjResidues: 1-801 converts the geranylgeranyl diphosphate into copalyl diphosphate AjBethway: the first step of the gibberellin biosynthesis	Query Match Best Local Similarity 34.2%; Pred. No. 1.94-81; Rest Local Similarity 34.2%; Pred. No. 1.94-81; Best Local Similarity 34.2%; Pred. No. 1.94-81; Matches 297; Conservative 171; Mismatches 307; Indels 94; Gaps 22; Qy 19 VPFRQSTNILIPFHKRSSFGFNAQHCVRSHLRLRMNCVGIHASAAETRPDQLPQEERPVS 78 11 LPSSSSLFFLHPFYKSSSLGAVSFVAKDKEKRCRAIS 47 Qy 79 RLNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKRIQT-LVKEIQCMFQSMGDGET 137 Qy 79 RLNADYHPAVWKDPFIDSLTSPNSHATSKSSVDETINKRIQT-LVKEIQCMFQSMGDGET 137 Qy 138 NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVINTLACL 197 Qy 138 NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVINTLACL 197 Qy 138 NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVINTLACL 197
DD 513 MPYVNNNGYLELAKQDYNNCQAQHQLEWDIFQKWYEENRLSEWGVRRSELLECYYLAAAT 572 QY 601 MFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLD- 652	RESULT 2 T02959 Yeaurene synthase A - maize C;Species: Zea may6 (malze) C;Species: Zea may6 (malze) C;Species: Zea may6 (malze) C;Species: Zea may6 (malze) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999 C;Accession: T02959 R;Bensen, R.J.; Johal, G.S.; Crane, V.C.; Toseberg, J.T.; Schnable, P.S.; Meeley, R.B.; R;Bensen, R.J.; Johal, G.S.; Crane, V.C.; Toseberg, J.T.; Schnable, P.S.; Meeley, R.B.; R;Ateference number: Z14794; MUID:95210929; PMID:7696880 A;Accession: T02959 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-823 < RBBNA A;Residues: 1-823 < RBBNA A;Residues: 1-823 < RBBNA A;Generics: ANI C;Function:	A; Description: cyclase involved in gibberelic acid blosymenests Query Match 28.4*; Score 1318; DB 2; Length 823; Best Local Similarity 35.0*; Pred. No. 1.9e-82; Matches 302; Conservative 157; Mismatches 275; Indels 130; Gaps 26; Qy 71 POBERFVSRLNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINK	147 147 203 207 267 267 352 326

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853
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                                                                                                                                                                                                                                                                                                                                                                153 IDGSGAPQFPQTLQWILNNQLPDGSWG---EECIFLAYDRVLNTLACLLTLKIWNKGDIQ
                                                                                                                                                                                                                                                                                                                                                                                         PSSQNAPLFPQCVKWLLDNQHEDGSWGLDNHDHQSLKKDVLSSTLALKKWGIGERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLDEAKSLGLDLPYHLPFISQIHQKRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                     26;
                                                                                                                                                                 Query Match
22.3%; Score 1034; DB 2; Length 7
Best Local Similarity 32.4%; Pred. No. 5.9e-63;
Matches 259; Conservative 156; Mismatches 329; Indels
A;Molecule type: mRNA
A;Residues: 1-785 <YAM>
A;Cross-references: EMBL:AF034774; PIDN:AAC39443.1
C;Genetics:
A;Gene: GA2
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TSNDLMSLVKSVIYEPVS 778
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LIGPPLPE---KTVDSHQXNQLYKLVSTMGRLLNDIQGFKRESABGKL-NAVSLHMKHER
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RESULT 6 G96825 hypothetical protein TBK14.12 [imported] - Arabidopsis thaliana G:Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 02-Mar-2001 #sequence_revision 02-Mar-2001

C;Accession: G96825
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authers Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Accession: G96825
A;Accession: G96825
A;Accession: G96825 737 644 FTGELLPDYILQQVDLR--SKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCYNR-EN 794 NNVOALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFAACRIAYAKTS 617 524 677 584 446 IGVIDN----LNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALA---KNNAFDKWAVKKDL 499 407 557 245 305 329 209 PSSQNAPLFPQCVKWLLDNQHEDGSWGLDNHDHQSLKKDVLSSTLASILALKKWGIGERQ 126 269 99 A;Cross-references: GB:AE005173, NID:g4835764; PIDN:AAD30231.1; GSPDB:GN00141 C;Genetics: LKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKXVPTFNEYVENAKVSIALATVVLNSIF CLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNTVNGFGKDG ---DAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLENFRDEKGDFFCFAGGTQ 330 KRCLHFLMFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRYFKKEIKESLDYVRYW 246 DGCLRYLCSILQKFRAAVPSVYPFDQYARLSIIVTLESLGIDRDFRTEIKSILDETYRYW 306 LRGDEBICLDLATC------FSDTL PGEVEYAIKYPWHRSMPRLEARSYIEQFGS--NDVWLGKTVYKMLYVSNEKYLELAKLDF 153 IDGSGAPOFPOTLOWILNNOLPDGSWG---EBCIFLAYDRVLNTLACLLTLKIWNKGDIO KKLOKIPLNVLHNHQTALLYSLEGLODVVDWQEITNLQSRDGSFLSSPASTACVFMHTON 98 TSPNSHATSKSSVDETINKR----IQTLVKEIQCMFOSMGDGETNPSAYDTAWVARIPS **VQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLDEAKSLGLDLPYHLPFISQIHQKRQ** 26; Indela Length 22.2%; Score 1033; DB 2; 32.4%; Pred. No. 7e-63; iive 156; Mismatches 329; 22.2%; Sc Query Match Best Local Similarity 32.4%; Pri Matches 259; Conservative 156; A;Status: preliminary A;Molecule type: DNA A;Residues: 1-785 <STO> A;Gene: T8K14.12 A;Map position: 1 447 352 525 678 390 558 465 618 200 408 67 127 270 186 7 g ઠ a 8 a 8 ð 셤 ઠે 셤 ò 요 g 셤 ò ద ઠે 셤 ò ò

OY 795 PECTEEBALSHVYGIIDNALKELN-WELANPASNAPLCVRRLLFNTARVMQLFYMYRDGF 853	Db 437 LKHLDHRMWIEDKNSNVLSMEKASFLRLHSSYSDKLTHLAARNFEPQQAKYCRELEEL 494 Qy 574 WWRESGFNDLTFTRQRPVEMYFSVAVŞM-FEPEFAACRIAYAKŢSCLAVILDDLYDTHGS 632
Qy 854 GISDKEMKDHVSRTLFDPVA 873	Db 495TIEKTTYCYFATVTSLPYEYAIKFGKLA-AKTAILITIADDFFDEKGS 541
Db 761TSNDLMSLVKSVIYEPVS 778	QY 633 LDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNTVNGFGKDGLKEGGRDVLGYLRKV 692
RESULT 7 A96637 hypothetical protein F11P17.15 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)	Qy 693 WEGLIASYTKEAEWSAAKYVPTFNEYVENAKVSIALATVVINSIFFTGELLPDYILQOVD 752
C;Date: 02-Mar-2001 #Bequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A96637 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;	QY 753 LRSKPLHLVSLTGRLINDTKTYQAERNRGELVSSVQCYMRENPECTEEBALSHVYGIIDN 812
ansen, N.F.; Hugnes, B.; Hulzar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	QY 813 ALKE-LNWELANPASNAPLCVRRLLFNTARVMQLFYMYRDGRGISDKEMKDHVSRTLFDP 871
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authores Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712	Qy 872 V 872 Db 775 I 775
A;Accession: Asos; A;Status: preliminary A;Molecule type: DNA A;Residues: 1-870 <sto></sto>	RESULT 8 A56118 vetispiradiene synthase 1 - Hyoscyamus muticus (fragment)
A;Cross-references: GB:AE005173; NID:g2443889; PIDN:AAB71482.1; GSPDB:GN00141 C;Genetics: A;Gene: F11P17.15 A:Man nomition: 1	C;Species: Hyoscyamus muticus C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 29-Sep-1999 C;Accession: A56118
Query Match 15.2%; Score 705; DB 2; Length 870; Best Local Similarity 27.1%; Pred. No. 2.9e-40; Matches 228; Conservative 160; Mismatches 311; Indels 142; Gaps 33;	A. Biol. Chem. 270, 735-7381, 1995 A.Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus mu- A. Reference number: AS6118; MUID:95221394; PMID:7706281 A. Accession: A56118
PQSMGDGETNPSAYDTAWVARIPS-1 	A;Status: preliminary A;Molecule type: mRNA A;Residus: 1-520 <bac> A;Cross-references: GB:UZ0188; NID:9763422; PIDN:AAA86337.1; PID:9763423</bac>
QY 153IDGSGAPQFPQTLQMILNNQ-LPDGSWGBECIFLAYDRV 190 DD 53 INVDDNELKPMFQGCLDWIMCNQNAREGFWMNSTSYTTVADGRDEDGEKDMCIL 106	C;Superramily: vetispiradiene synthase 1 Query Match Best Local Similarity 27.2%; Pred. No. 1e-37;
Qy 191 LNTLACLLTLKIWNKGDIQVQKGVEPVRKHMEEMKDEADNHRPSGFEVVPPAMLDEA 247	Matches 157; Conservative 130; Mismatches 216; Indels 74; Gaps 12; Qy 301 QEITNLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDFFRLW 360
Qy 248 KSLGLDLPYHLPPISQIHQKRQKKLQKIPLNVLHNHQTALLYSLBGLQ 295 1	11 QEISTLKEQTSTWLSAACGTTTTEKLN 361 AVDTVERLGIDRYFKKEIKESLDYVRYWDAERGVGWARCNPIPDVDDTAMGLRILR : : : :
QY 296 DVVDWQBITNLQSRDGSFLSSPASTACVFWHTQNKRCLHFLNFVLSKFGDYVPCHYPL 353 :	
Qy 354 DLFERLWAVDTVERLGIDRYFKKEIKESLDYVY-RYWDAERGVGWARCNPIPDVDD 408	89 QHGXNVSFNIFSKFQDANGKFKKSLKSDIKGLLNLYEASHVKTHKEDILEEALVFSV 478 NHLQNALAKQNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKT 1
Qy 409TAMGLRILRLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDNLNLYR 457 :	146 538
Qy 458 CSQVCFPGEKIMEBAKTFTTNHLQNALAKNNAFDKWAVKKDLPGEVEYAIKYFWHRS 514 : : :	DD 186 IYEEEFFKNDLLLARFAKLDYNLLQMLHKHELSEVSRWWKDLDFYTTLPYARDRAVECYFW 245 QY 597 VAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRD 656 ::: : : : : :: :: :: :: :: :: ::::
Oy 515 MPRLEARSYIEQFGSNDVWLGKTVYKMLYVS-NEKYLELAKLDFNMVQALHQKETQHIVS 573	Db 246 TMGVYAEPQYSQARVMLAKTIAMISIVDDTFDAYGIVKELEVYTDAIQRWDISQIDRLPE 305 Qy 657 NQLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFN 716

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probable limonene cyclase - Arabidopsis thaliana probable limonene cyclase - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000

C;Accession: F71434

C;Accession: F71434

P; Wedler, H; Wedler, E; Wambutt, R; Weitzenegger, T; Pohl, T.M; Terryn, N; Gie P; Wedler, H; Wedler, E; Wambutt, R; Weitzenegger, T; Pohl, T.M; Terryn, N; Gie P; Wedler, H; Wedler, B; Stoter, P; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1988

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Punk, B.

C; Chalwastzis, N.

C; Chalwastzis, N.

A;Attle: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha A;Reference number: A71400; MUID:9812113; PMID:9461215

A;Accession: F71434

A;Attle: Analysis of 1.9 Mc Contiguous sequence from chromosome 4 of Arabidopsis tha A;Reference number: A71401; MID:9812113; PMID:9461215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-600 <BEV>A;Residues: 1-600 <BEV>A;Cross-references: GB:Z97341; NID:g2244991; PID:g2245028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 TINHLQNALAKNNAFDKWAVKKD---LPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDV
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14.1%; Score 654.5; DB 2;
Best Local Similarity 31.1%; Pred. No. 5e-37;
Matches 164; Conservative 105; Mismatches 210;
843 MOLFYMYRDGFGISDKEMKDHVSRTLFDPVA 873
                             A;Map position: 4COP9-4G3845
C;Superfamily: vetispiradiene synthase 1
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Jimonene cyclase - spearmint

C;Species: Mentha spicata (spearmint)

C;Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

C;Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

C;Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

C;Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

B;Colby, S.M.; A48863

A;Title: 45-Imfonene synthase from the oil glands of spearmint (Mentha spicata). cDNA

A;Reference number: A48863; MUID:94043077; PMID:8226816

A;Status: preliminary
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                                                                                                                                   ERNRGELVSSVQCYMRENPECTEEEALSHVYGIIDNALKELNWELANPASNAPLCVRRLL 836
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Best Local Similarity 31.0%; Pred. No. 2.1e-37;
Matches 177; Conservative 101; Mismatches 219; Indels 74; Gaps
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A,Residues: 1-599 <COL»
A,Cross-trences: GB:L13459; NID:g410229; PIDN:AAC37366.1; PID:g410230
C;Superfamily: vetispiradiene synthase 1
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R;Chen, X.Y.; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a ca A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a,Reference number: S68365
A;Accession: S68365
A;Accession: S68365
A;Residues: 1-554 <CHE>
A;Residues: 1-554 <CHE>
A;Cross-references: EMBL:U23206; NID:g1045311; PIDN:AAA93064.1; PID:g1045312
A;Cross-references: Cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin biosynthesis
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C;Species: Gossypium arboreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C;Accession: S68366
R;Chen, X X; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch. Biochem: Biophys: 324, 255-266, 1995
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a ca
A;Reference number: S68365; MUID:96132653; PMID:8554317
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A;Molecule type: mRNA
A;Residues: 1-554 <CHIS>
A;Cross-references: EMBL:U23205; NID:g1045313; PIDN:AAA93065.1; PID:g1045314
A;Experimental source: cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 103; Mismatches 210;
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Pred. No. 2.5e-36;
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Best Local Similarity
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Matches 162;
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R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Punk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
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GIIGVAWDDLNMEKKS------CRLHQGFLEAAANLGRVAQCYYQYGDGHGCPDKAKTV 508
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Bate: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
R;Bevan, M.: Bancroft r.n.--
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C;Accession: S68365
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A;Cross-references: GB:Z97341; NID:G2244991; PID:e327011; PID:G2245029
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Best Local Similarity 32.84
Matches 179; Conservative
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C;Genetics:
A;Map position: 4COP9-4G3845
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seguiterpene cyclase (EC 2.5.1.-) - pepper esgquiterpene cyclase (EC 2.5.1.-) - pepper esgquiterpene cyclase (EC 2.5.1.-) - pepper c;species: Capaicum annuum (pepper)
C;species: 10-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: 108174
R;Back, K; Shin, D.H.; He, S.
R;Back, K; Shin, D.H.; He, S.
Plant Cell Physiol. 39, 899-904, 1998
A;Title: Cloning and bacterial expression of sesquiterpene cyclase, a key branch point A;Reference number: 216395; MUID:99033462; PMID:9816674
A;Accession: T08174
A;Accession: T08174
A;Reference number: 216395; MUID:9903342; PIDN:AAC61260.1; PID:93108343
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                                                                                                                                                                     654 VRDNQLKVCFLGLYNTVNGFGKDGLKEQGRD-VLGYLRKVWEGLLASYTKEAEWSAAKYV
                                                                                                                                                                                                                                                                                                                                             PTFNEYVENAKVSIALATVVLNSIFFTGEL----LPDYILQQVDLRSKFLHLVSLTGRLI
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FTTNHLQNALAKNNAPDKWAVKKDLPGEVEYALKYPWHRSMPRLEARSYIEQFGSNDVWL
                        29;
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13.6%; Score 633.5; DB 2;
Best Local Similarity 30.7%; Pred. No. 1.2e-35;
Matches 163; Conservative 107; Mismatches 202;
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Superfamily: vetispiradiene synthase 1
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R;Facchini, P.J.; Chappell, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11088-11092, 1992
A;Title: Gene family for an elicitor-induced sesquiterpene cyclase in tobacco. A;Reference number: Z15024; MUD:93066390; PMID:1438319
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-550 <FAC>
A;Residues: 1-550 <FAC>
A;Cross-references: EMBL:L04680; NID:g170342; PIDN:AAA19216.1; PID:g505588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWLGKTVYKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGF-NDLTFTRQRP
                                                                                                                          LRLHGYNVSSDVLENFRDEKGDFFCFAGOTOIGVTDN----LNLYRCSQVCFPGEKIMBE
                                                                                                                                                          AKTETTNHLONALAKNNAPDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSND
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174 AISFTTNHLSLAVA-----SLDYPLSEEVSHALKQSIRRGLPRVEARHYL----
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Best Local Similarity 29.0%; Pred. No. 1.2e-35; Length 550; Matches 153; Conservative 118; Mismatches 203; Indels 53.
    47;
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      Indels
    103; Mismatches 212;
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         161, Conservative
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요 ò

Search completed: August 17, 2004, 21:03:06 Job time : 23.2551 secs

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                     methanococc
homo sapien
                                             mus musculu
                                                      arabidopsis
                                                                     caulobacter
                                                                                b replicase
b replicase
                                                                                                        arabidopsis
                                                                                                                   homo sapien
                                                                                                                                           homo sapien
        caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINGE-1199728; PubMed=11404343;
Trapp S.C., Croteau R.B.;
"Genomic organization of plant terpene synthases and molecular
"Genomic organization of plant terpene synthases and molecular
genetics 158:811-832(2001).
-!-FUNCTION: Catalylyses the cyclization of the ubiquitous isoprenoid
intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
parent olefin with a taxane skeleton.
-!-CATALYNIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene
diphosphate.
-!-ATALWIY Taxol biosynthesis; first step.
-!-SIMILARITY: Belongs to the terpene synthase family.
                                                                                                                                                                                                                 RESULT 1
TASY TAXBR STANDARD; PRT; 862 AA.

AC G41554; Q94FV8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annocation update)
DT 28-FEB-2003 (Rel. 41, Last annocation update)
DT 28-FEB-2003 (Rel. 41, Last annocation update)
DT 28-FEB-2003 (Rel. 41, Last annocation update)
                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
NCBI_TaxID=46220;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-96199163; PubMed=8621577;
Wildung M.R., Croteau R.B.;
A.c.DMA clone for taxadiene synthase, the diterpene cyclase that catalyzes the committed step of taxol biosynthesis.";
J. Biol. Chem. 271:9201-9204(1996).
                              Q8wxh0
Q9wvf7
Q9sjp6
P52977
Q801a29
Q80439
P38605
Q90650
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SIMILARITY.
SIMILARITY.
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                    SMC METUA
DPOE MOUSE
FUIO ARATH
LION CAUCR
RIAB CVBEN
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InterPro; IRR008930; Terp cyc toroid.
InterPro; IRR001906; Terp cyc toroid.
InterPro; IRR001906; Terp cyc toroid.
InterPro; IRR008949; Terpene synth C.
InterPro; IRR008949; Terpene synth, C.
Pfam; PR01397; Terpene synth; I.
Pfam; PR01395; Terpene synth, C; I.
Taxol biosynthesis; Lyase.
DYHC CAL
METUA
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EMBL; AF326519; AAK83566.1; -.
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       1169
6885
2283
440
7094
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2220
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ACT SITE
        Q41594 taxus brevi
Q91437 taxus chine
Q22340 abies grand
Q24475 abies grand
Q24475 abies grand
Q29761 gossypium a
Q49537 nicotiana a
Q49537 nicotiana a
Q40577 nicotiana a
Q40577 nicotiana a
P59265 gossypium a
Q40577 ricinus com
P55287 ricinus com
P55287 ricinus com
P5528 rhizobium a
Q40577 nicotiana a
P59287 ricinus com
P5528 niconius a
Q4057 nicotiana a
Q4057 metadyrhizob
P11029 gallus gall
Q80xk6 mus musculu
Q80xk6 mus musculu
Q80xk drosophia
Q564373 claviceps p
Q5048k2 drosophia
Q56547 homo sapien
P55433 buchnera ap
Q60507 methanococc
P5747 buchnera ap
Q60107 methanococc
Q6111 bacceriopha
Q87786 thermoaner
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                                                                                      August 17, 2004, 20:56:14; Search time 10.7844 Seconds (without alignments) 4215.079 Million cell updates/sec
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                                                                                                                                                               1 MAGVLPANLPCSLQLSPKVP.....GISDKEMKDHVSRTLPDPVA 873
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Q28559 0
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          141681 seqs, 52070155 residues
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TSD2 ABIGR
TSD1 ABIGR
DCS1 GOSAR
DCS2 GOSAR
SEAS TOBAC
DCS3 GOSAR
DCS1 GOSAR
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VL49 BRAJA
VL49 BRAJA
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                   AAETRP---DOLPQEERFVSRLNADYHPAVWKDDFIDSLTSPNSHATSKSSVDETINKRI 118
                                                                                            DIKTY OA ERNRGELVSSVOCYMRENPECTEBEALSHVYGII DNALKELNWELANPASNAP
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                                            Indels
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167 A -> V (IN REF. 2).
98303 MW, 9141B59780CD79A1 CRC64;
                              42.2%; Score 1959; DB 1; 1
11 Similarity 43.6%; Pred. No. 4.9e-126;
385; Conservative 167; Mismatches 255;
                                                          33 KRSSFGFNAOH----C-VRSHLRLRWNC-----
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BIIFPALLQKAKALGINLPYDLPFIKSLSTTREARLTDVSAAADNIPANMLN------
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                                                synthase)
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene TDC1 OR TASY.
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B37835AFFDC1DEFE CRC64;
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43.3%; Pred. No. 4.4e-125;
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InterPro; IPR00930; Terp_cyc_toroid.
InterPro; IPR001906; Terpene synth-like.
InterPro; IPR008949; Terpene synth_C.
InterPro; IPR008949; Terpene synth_C.
Pfam; PF01397; Terpene synth; I.
Pfam; PF0336; Terpene synth; I.
Taxol biosynthesis; Lyase.
ACT_SITE 938 835 BY SIMILAR
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"Cloning, expression, and characterization of taxadiene synthase, a diterone cyclase from Taxus chinensis.";
Submitted (AUG-2000) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid intermediate geranylgeranyl diphosphate to taxa-4,11-diene, parent olefin with a taxane skeleton.
-!- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene diphosphate.
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8-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Taxaceae, Taxus.
NCBI_TaxID=29808,
                                                                                                                                                                                                                                                                                                                          PATHWAY: Taxol biosynthesis; first step. SIMILARITY: Belongs to the terpene synthase family.
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InterPro; IPR008930; Terp_cyc_toroid.
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al Similarity 45.0%; Pred. No. 4.9e-123;
370; Conservative 165; Mismatches 245; Indels
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3A597BAF722BF679 CRC64;
LATO; IPR001906; Terp_synth-like.
LATERPRO; IPR005630; Terpene synth C.
DR Pfam; PR0139; Terpene synth; I.
DR Pfam; PP01397; Terpene synth; I.
DR Taxol biosynthesis; Lyase.
FT ACT SITE 758 758
FT ACT SITE 835 P.
SEQUENCE 3 SEQUENCE
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us-10-041-007-2.rsp

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EMBL; U87908; AAB71084.1; -.
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SEQUENCE FROM N.A., AND CHARACTERIZATION.

MEDLINE-97413772; PubMed=9268308;

A Bohlmann J., Steele C.L., Croteau R.;

Bohlmann J., Steele C.L., Croteau R.;

Bohlmann J., Steele G.L., Croteau R.;

Characterization, and functional expression of myrcene synthase, (-)-

(4S)-limonene synthase, and (-)-(15,5S)-pinene synthase.";

J. Biol. (Chem. 277:21784-21792(1997).

C. - FUNCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene (C10) olefins blosynthesis.

C. - CATALYTIC ACTIVITY: Geranyl diphosphate = limonene + diphosphate.

C. - CATALYTIC ACTIVITY: Geranyl diphosphate = limonene + diphosphate.

C. - CATALYTIC ACTIVITY: Geranyl diphosphate.

C. - CATALYTIC ACTIVITY: Geranyl diphosphate.

C. - CATALYTIC ACTIVITY: Geranyl diphosphate.

C. - CATALYTIC STORIENIAN: Oleocresinosis.

C. - INDUCTION: By wounding.

C. - INDUCTION: By wounding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAKTFTTNHLQNALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSN
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                                                                                               Abies grandis (Grand fir).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Abies.
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25.7%; Score 1194.5; DB 1; Length 637;
Best Local Similarity 41.9%; Pred. No. 5.5e-74;
Matches 244; Conservative 117; Mismatches 187; Indels 35;
                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
(-)-(4S)-limonene synthase, chloroplast precursor (EC 4.2.3.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AFO06193; AAB70907.1; -.

EMBL, AFO06193; AAB70907.1; -.

InterPro; IPR001906; Terp_synth-like.

InterPro; IPR001906; Terpene synth C.

InterPro; IPR008949; Terpene synth C.

R InterPro; IPR008949; Terpene synth J.

R Pfam; PF001396; Terpene synth J.

I Lyase; Manganese; Transit peptide; Chloroplast.

I TRANSIT 7 CHAIN 7 637 CHAOPOLAST (POTENTIAL).

I ACT SITE 533 533 BY SIMILARITY.

ACT SITE 610 610 BY SIMILARITY.

I ACT SITE 614 614 BY SIMILARITY.

R SEQUENCE 637 AA; 73477 MW; BEBOCD9DDE886898 CRC64;
   STANDARD;
                                                                                                                                                NCBI_TaxID=46611;
    rsd3 ABIGR
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                          298 GY---ESLNEMPYMANKKLLQLAKLEFNIFHSLQLRELQSISRWWKESGSSQLTFTRHRH 354
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopeida; Coniferales; Pinaceae; Abies.
VCBI_TaxID=46611;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myrcene synthase, chloroplast precursor (EC 4.2.3.15).
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InterPro; IPR001906; Terp_synth-like.
InterPro; IPR005630; Terpene synth_C.
InterPro; IPR008949; Terpenoid_synth.
Pfam; PP01397; Terpene_synth; 1.
Pfam; PP03936; Terpene_synth_C; 1.
Iyase; Manganese; Transit peptide; Chloroplast.
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Ad3.18.
Ables grandis (Grand fir).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
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                                                                                                                                       241 IFSTRYLKEALQK-----IPVSALSQEIKFVMEYGWHTNLPRLEARNYIDTLEKDTSA
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                                                                                            DLFERLWAVDTVERLGI DRYFKKEI KESLDYVYRYWDAERGVGWARCNPI PDVDDTAMGL
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                                                             DB 1; Length 627;
                                                                             224; Conservative 104; Mismatches 173; Indels
            MYRCENE SYNTHASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
', ZEODA492EOC971FD CRC64;
     CHLOROPLAST (POTENTIAL)
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                                                            Score 1167.5; DB Pred. No. 3.7e-72
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 PL-DLFERLWAVDTVERLGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTA
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    diphosphate.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 24.8%; Score 1151.5; DB 1; Length Best Local Similarity 44.0%; Pred. No. 4.7e-71; Matches 230; Conservative 97; Mismatches 179; Indels
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                                                                                                      INDUCTION: By wounding.
SIMILARITY: Belongs to the terpene synthase family
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InterPro; IPR008930; Terp_cyc_toroid.
InterPro; IPR001906; Terp_synth-like.
InterPro; IPR008949; Terpene, synth C.
InterPro; IPR008949; Terpenoid synth.
Fam, PP01397; Terpene synth C; 1.
Lyase; Manganese; Transit peptide; Chloroplast.
TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
CHAIN ? 628 PINENE SYNTHASE.
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produced by this enzyme. CATALYTIC ACTIVITY: Geranyl diphosphate COFACTOR: Manganese and potassium.
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                                                             PATHWAY: Oleoresinosis. SUBCELLULAR LOCATION: Chloroplast.
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HSSP: 040577; SRAT.
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                                                                                                                                             710 KYVPTFNEYVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSLTGRLIN 769
                                                                                                VEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISV 650
                      LDSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDV-LGYLRKVWEGLLASYTKEAEWSAA
                                                                                                                                                                    770 DIKTYQABRARGELVSSVQCYMRENPECTEEFALSHVYGIIDNALKELAWFLANPASNAP
                                                                                                                                                                                                                                          Gossypium arboreum (Tree cotton).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
euroaida II, Malvales; Malvaceae; Malvoideae; Gossypium.
NCBI_TaxID=29729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase isozyme XC14 (BC 4.2.3.13) (D-cadinene
                                                                                                                                                                                                                                                                                             830 LCVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 873
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BY SIMILARITY.
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InterPro; IPR001906; Terp_synth-like.
InterPro; IPR001906; Terp_synth-like.
InterPro; IPR001906; Terpene synth C.
InterPro; IPR001949; Terpene synth C.
InterPro; IPR001949; Terpene synth C; 1.
Ivase; Multiqene family. BY SIMILARI ACT_SITE 57 57 57 BY SIMILARI ACT_SITE 531 531 BY SIMILARI SEQUENCE 554 AA; 64158 MW; A88974665
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HSSP; Q40577; SEAU.
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STRAIN=CV. Nanking;
STRAIN=S012653; PubMed=8554317;
STRAIN=912653; PubMed=8554317;
Chen X.-Y., Chen Y., Heinstein P., Davisson V.J.;
Choing, expression, and characterization of (+)-delta-cadinene synthase: a catalyse for cotton phycoalexin biosynthesis.";
Arch. Biochem. Biophys. 324:255-266(1995).
I-FUNCTION: Responsible for the cyclization of trans, trans-farnesyl diphosphate (FPP) to (+)-delta cadinene.
I-CAPALYTIC ACTIVITY: 2-trans, 6-trans-farnesyl diphosphate = (+)-delta-cadinene + diphosphate.
I-PATHMAY: Phytoalexins gossypol and lacinilene C biosynthesis;
first (committed) step.
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                                                                                                                                                     Gossypium arboreum (Tree cotton).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                  Query Match
13.9%; Score 647.5; DB 1; Length 554;
Best Local Similarity 30.9%; Pred. No. 1.1e-36;
Matches 162; Conservative 103; Mismatches 210; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: Belongs to the terpene synthase family.
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527 527 BY SIMILARITY.
531 531 BY SIMILARITY.
554 AA, 64137 MW, 59D6922BDF9DCAF CRC64;
                                                              554 AA
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InterPro; IRR008930; Terp_cyc_toroid.
InterPro; IRR001906; Terp_synth-like.
InterPro; IRR001906; Terpene synth_C.
InterPro; IRR008949; Terpenoid synth. Effam; PRO1397; Terpene_synth; I.
Pfam; PRO3936; Terpene_synth, I.
Lyase; Multigene family.
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                                                                                                             AKTFTTNHLQNALAKNNAPDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. Nanking;
STRAIN=CV. Nanking;
Meng Y., Jia J., Liu C., Liang W., Zhou X., Heinstein P., Chen X.-Y.;
Submitted (FEB-1996) to the EMBL/GenBank/DBBJ databases.
-! FUNCTION: Responsible for the cyclication of trans, trans-farnesyl
diphosphate (FPB) to (+)-delta cadinene.
-! CATALYTIC ACTIVITY: 2-trans, 6-trans-farnesyl diphosphate = (+)-
delta-cadinene + diphosphate.
-!- PATHWAX: Phytoallexins gossypol and lacinilene C biosynthesis;
first (committed) step.
-!- SIMILARITY: Belongs to the terpene synthase family.
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                                  Gaps
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Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
NCBI_TAXID=29729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase isozyme C2 (EC 4.2.3.13) (D-cadinene
                                47;
          Length 554;
                               Indels
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Matches 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKTFTTNHLONALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVAEHKPKHRREDDCSAIECYMEEYGVSAQE----AYDVFNKHVESAWKDVNQEFQKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREHGYNVSCDVFNKFKDEQGNF-----KSSVTSDVQGLLELYQASYLRVHGEDILDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEMYPSVAVSMPEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERLWAVDTVERLGIDRYFKKEIKESLDYVY-RYWDAERGVGWARCNPIPDVDDTAMGLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDN----LNLYRCSQVCFPGEKIMEE
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 43, Last annotation update)
Aristolchene synthase (EC 4.2.3.9) (5-epi-aristolochene synthase)
(EAS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.9%; Score 643.5; DB 1; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNAPLCVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA
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35DDD66D3E838AAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2e-36;
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                InterPro; IPR008930; Terp_cyc_toroid. InterPro; IRR001906; Terp_gynth.like. InterPro; IPR001906; Terppene synth.C InterPro; IPR008949; Terpenoid synth.Pfam; PF01397; Terpene synth; I. Pfam; PF03936; Terpene synth; I. Lyase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                   BY
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BY
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                                                                                                                                EMBL; Y16432; CAA76223.1; -. HSSP; Q40577; 5EAU.
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                                                                                                                                                                                                                                                                                                                                                                                                                   531 5
554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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353 LDLFERLWAVDTVERLGIDRYFKKEIKESLDYVYRYMDAERGVGWARCNPIPDVDDTAWG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 FRLLRQHGFNISPEIFSKFQDENGKFKESLASDVLGL---LNLYBASHVRTHADDILEDA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 LAFSTIHLESAAPH-----LKSPLREQVTHALEQCLHKGVPRVETRFFI-----
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Best Local Similarity 28.9%; Pred. No. 5.9e-36;
Matches 153; Conservative 119; Mismatches 204; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62973 MW; 9FE1C59CF1A68BF1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 56-73.
STRAIN-cv. NK326;
MEDLINE-93066390; Pubmed=1438319;
Pacchini P.J., Chappell J.;
"Gene family for an elicitor-induced sesquiterpene cyclase in
                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 89:11088-11092(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTON ACCEPTOR.
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PIR; T03714; T03714.
PDB; 5EA3; 15-0CT-97.
PDB; SEA7; 12-NOV-97.
PDB; SEA7; 12-NOV-97.
PDB; SEA7; 12-NOV-97.
InterPro; 1PR001906; Terp_synth-1ke.
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InterPro; 1PR01906; Terpene_synth_C.
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          NCBI_TaxID=4097;
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12; 410

Gaps

45;

DB 1; Length 555;

589

273

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68 DSNQKLPPIDAVQRLGVSYHFEKEIEDELENIYRDTNNNDAD-----TDLYTTA 116
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                                                                                                                                                           al Similarity 30.3%; Pred. No. 1.3e-35; 159; Conservative 104; Mismatches 217; Indels
BY SIMILARITY.
7060C4F9D99412F9 CRC64;
                                        64103 MW;
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                                                                             DSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRD-VLGYLRKVWEGLLASYTKEAEWSAAK 710
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MEDLINE=97060798; PubMed=8904844;
MEDLINE=97060798; PubMed=8904844;
Cloning and heterologous expression of a second (+)-delta-cadinene synthase from Gossypium arboreum.";
J. Nat. Prod. 59:944-551[1996]
J. Nat. Prod. 59:944-551[1996]
J. Holling and heterologous expression of a second (+)-delta-cadinene synthase from Gossypium arboreum.";
J. Nat. Prod. 59:944-551[1996]
J. Nat. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod. Prod
                                    EMYPSVAVSMPEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVL
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
NCBI_TaxID=29729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PATHWAY: Phytoalexing gossypol and lacinilene C biosynthesis, first (committed) step.
-1- SIMILARITY: Belongs to the terpene synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR.2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase isozyme A (EC 4.2.3.13) (D-cadinene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAPLCVRRL--LFNTARVMQLFYMYR-DGFGISDKEMKDHVSRTLFDPV 872
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InterPro; IPR001906; Terp synth-like.
InterPro; IPR001906; Terpens synth. C.
InterPro; IPR008949; Terpenoid synth.
Pfam; PP01397; Terpene_synth; I.
Lyase; Multigene family.
ACT_SITE 452 BY SIMILAR:
ACT_SITE 528 S28 BY SIMILAR:
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FUNCTION: Responsible for the cyclization of trans, trans-farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gossypium hirsutum (Upland cotton).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-WAR-2D04 (Rel. 43, Last annotation update)
(+) -delta-cadinene synthase (RC 4.2.3.13) (D-cadinene synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96351891; PubMed=8728715;
Davis E.M., Tsuji J., Davis G.D., Pierce M.L., Essenberg M.;
"Purification of (+)-delta-cadinene synthase, a sesquiterpene
from bacteria-inoculated cotton foliar tissue.";
Phytochemistry 41:1047-1055(1996).
--- FUNCTION: Responsible for the cyclization of trans,trans-f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Westburn M;
Davis B.M., Chen Y.-S., Essenberg M., Pierce M.L.;
"CDNA sequence of a (+)-delta-cadinene synthase gene induced
Gossypium hirsutum L. by bacterial infection.";
(In) Plant Gene Register PGR98-040.
554 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE, AND CHARACTERIZATION.
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601 AA

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STANDARD;
                                                                                                                                                                                                                            NCBI_TaxID=3988;
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                                                         28-FEB-2003
28-FEB-2003
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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    771 TKTYQAERNRGELVSSVQCYMRENPECTEERALSHVYGIIDNALKELNWELANPASNAPL 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDV-LGYLRKVWEGLLASYTKEAEWSAAK 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVPTENEXVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSLTGRLIND 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIHGYNVSSDVLENFRDEKGDFFCFAGOTQIGVTDN----INLYRCSQVCFPGEKIMEEA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 KEHGFHVSCDVFNKFKDEGGNF-----KSSVTSDVRGLLELYQASYLRVHGEDILDEA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 WLGKTVYKMLYVSNEKYLELAKLDFNMVQALHOKETQHIVSWWRESGF-NDLTFTRQRPV
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    diphosphate (FPP) to (+)-delta cadinene.
CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+).
delta-cadinene + diphosphate.
PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 554;
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                                                                                          first (committed) step.
-!- INDUCTION: By bacterial infection.
-!- SIMILARITY: Belongs to the terpene synthase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.4%; Score 622.5; DB 1; Best Local Similarity 30.2%; Pred. No. 5.4e-35; Matches 158; Conservative 104; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    interPro; IPR008930; Terp_cyc_toroid.
InterPro; IPR001906; Terp_synth-like.
InterPro; IPR005430; Terpena synth.C.
InterPro; IPR008949; Terpenoid synth.
Pfam; PF01397; Terpene_synth; I.
Pfam; PF013936; Terpene_synth.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 451 BY
527 527 BX
531 531 BX
554 AA; 64019 MW; 8
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RESULT 13 CASS_RICCO

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                                                                                                                                                                                                                        SEGUENCE FROM N.A.
MEDLINE=94359958; PubMed=8078910;
MAU C.J., West C.A.;
"Cloning of casbene synthase CDNA: evidence for conserved structural features among terpenoid cyclases in plants.";
Proc. Natl. Acad. Sci. U.S.A. 91:8497-8501(1994).
                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Malpighiales, Euphorbiaceae, Acalyphoideae, Acalypheae,
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Conservative 112; Mismatches 209; Indels
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F7B362D286747957 CRC64;
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CASBENE SYNTHASE.
                                                         Casbene synthase, chloroplast precursor (EC 4.2.3.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast, Transit peptide
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               41, Last sequence update)
41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; Score 594.5; 27.6%; Pred. No. 5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 132134; -; NOT ANNOTATED CDS.
InterPro; IPR008930; Terp_cyc_toroid.
InterPro; IPR008930; Terp_synth-like.
InterPro; IPR005630; Terpene synth_C.
InterPro; IPR008649; Terpene synth_C.
Pfam; PF01397; Terpene synth; I.
Pfam; PF03936; Terpene synth; I.
Pfam; defense; Lyase; Chloroplast; Trans
                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=97115639; PubMed=8954576;
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                                                                                    Ricinus communis (Castor bean)
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STANDARD;
Query Match
Best Local Similarity
Matches 115; Conserv
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                                                                   OFGSNDVWLGKTVYKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGF-NDLT 584
                                                                                                                             644
                                                                                                                                          703
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                                                                                                                                                                                                                                         AEWSAAKYVPTFNEYVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSL 763
                                                                                                                                                                                                                                                           | | :: | :: | : | 434 AVWRDEGKIPSPDXLYNGSMTTGLPLVSTASFMGVQEITGLNEFQWLETNPKLSYASGA 493
                                                                                                                                                                                                                                                                                                 764 TGRLINDTKTYQAERNRGELVSSVQCYMRENPECTEEEALSHVYGIIDNALKELNWELAN 823
                                                                                                                                                                                                                                                                                                                 824 PASNAPLCVRR-----LLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 873
             EKIMEEAKT PTTNHLONALAKNNA FDKWAVKKOL PGEVEYAIKY PWHRSMPRLEARSYIE
                            267 LYEAD------IECRNETLIEFAKLDYNRVQLLHQQELCQFSKWWKDLNLASDIP
                                                                                                                            PTRORPVEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVR
                                                                                                                                                                                  RWDISVLDSVRDNOLKVCFLGLYNTVNGFGKDGLKEQGRDV-LGYLRKVWEGLLASYTKE
                                                                                                                                                                                                   "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-I- SIMILARITY: STRONG, TO B.JAPONICUM HYPOTHETICAL 55.4 KDa PROTEIN
IN CYPLI7 3* REGION (ORP7).
-!- SIMILARITY: Contains 2 PFTB repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E4BD8C45FB52DCEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
06-COT--2001 (Rel. 40, Last annotation update)
Hypothetical 64.4 kDa protein Y4KT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 AA
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Interpro; IPR008930; Terp.cyc_toroid.
Pfam; PF00432; prenyltrans; 2.
Hypothetical protein; Repeat; Plasmid.
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P55538;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          278 NVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGSFLSSPASTACVFMHT-----QNK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 AQLDARIGVRGIGPA-LHFAADADDTAVALCVIRIAGRDPAVDALRHF--EIGELF---- 327
                                                                                                                                                                                                                                                                                                                                                                                                 --LHSWEAWGTWPTAACPD-------DDGSIGISPAATAAWRAHAVTQGSTPQVG 216
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                                                                                                                  114 INKRIQTLVKEIQCMFQSMGD-GETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQ
                                                                                                                                                                             173 LPDGSWGEECIFLAYDRVLNTLACLLTLKIWNKGD-----IQVQKGVEFVRKHMEEMKD
                                                                                                                                                                                                                                                                    227 EADNHRPSGFEVVFPAMLDEAKSL--GLDLPYHLPFISQIHQKRQKKLQKI-----PL
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                                                  Gaps
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
4.9%; Score 227.5; DB 1; Length 516; 24.0%; Pred. No. 4.8e-08; arive 54; Mismatches 182; Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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"Cloning and mutagenesis of a cytochrome P-450 locus from
Bradyrhizobium japonicum that is expressed anaerobically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
LOCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein blr2149 (ORF7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appl. Environ. Microbiol. 59:4136-4142(1993)
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Biochim. Biophys. Acta 1398:243-255(1998).
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MEDLINE=98322110; PubMed=9655913;
                                               115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 DEADNHRPSGFEVVFPAMLDEAKSL--GLDLPYH---LPFISQIHQKRQKKLQKIPLNVL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 LPSGHPLLHSWEA-----WGTSPTTACPDDDGSIGISPAATAAWRAQAVTRGSTPQVGR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 CLHFLNF----VLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDRYFKKEIKESLDYVYR 387
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4.6%; Score 214.5; DB 1; Length 516;
Best Local Similarity 24.0%; Pred. No. 3.7e-07;
Matches 115; Conservative 52; Mismatches 185; Indels 127; Gaps
Tabata S.; "Complete genomic sequence of nitrogen-fixing symbiotic bacterium "Complete genomic sequence of nitrogen-fixing symbiotic bacterium bradyrhizobium japonicum USDA110."; "Bradyrhizobium japonicum USDA110."; "BNA Res. 9:189-197(2002). "INTARITY: Contains 2 PFTB repeats."
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PIR, 140214; 140214.

InterPro; IPR001330; Prenyltrans.

InterPro; IPR008330; Terp_cyc_toroid.

Pfam; PF00432; prenyltrans. 2.

Pfam; PF00432; prenyltrans. 2.

Pfam; PF00432; prenyltrans. 2.

REPEAT 45 86

REPEAT 41 443 PFTB 1.

CONFLICT 134 134 S -> W (IN REF. 1 AND 2).

CONFLICT 278 278 D -> E (IN REF. 1 AND 2).

SEQUENCE 516 AA; 55268 WW; D7A3A6D66860A761 CRC64;
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MEDLINE=21381193; Pubmed=11488601;
Schepmann H.G., Pang J., Matsuda S.P.T.;
"Cloning and characterization of Ginkgo biloba levopimaradiene "Cloning which catalyzes the first committed step in ginkgolide
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Arch. Biochem. Biophys. 392:263-269(2001).

EMBL; AR131704; AL109965.19. -

GO; GO:0016829; F:1yeas activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR008309; Terpene synth.C.

InterPro; IPR008309; Terpene synth.C.

InterPro; IPR00830; Terp.Cyc.Coroid.

InterPro; IPR001906; Terp synth.like.

Pfam; PP01397; Terpene synth.like.

Pfam; PP01397; Terpene synth.li.

Pfam; PP03936; Terpene synth.li.

SEQUENCE 873 AA; 100290 MW; P2C980BB19F9931E CRC64;
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Ginkgo biloba (Ginkgo).

Sukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae;

NCBI_TAXID=3311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Result g ug-10-041-007-2.rspt

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RNRGELVSSVQCYMRENPECTEBEALSHVYGI I DNALKELNWELANPASNAPLCVRRLLF
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Stoffer-Vogel B., Wildung M.R., Vogel G., Croteau R.B.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RMEL, U50768; AAB05407.1; -.
RHESP; Q40577; SEAS.
RGO; GO:0016829; F:1yase activity; IEA.
GO; GO:0018152; P:metabolism; IEA.
RICEPTO; IPR0001330; Preparl trans.
RILEPTO; IPR000830; Terpend synth.C.
RILEPTO; IPR000830; Terpend synth.C.
RILEPTO; IPR000830; Terpend synth.
RILEPTO; IPR000830; Terpend synth.
REPTO; IPR001306; Terp. Synth.
REPTO; IPR001306; Terp. Synth.
REPTO; IPR01397; Terpend synth.C.
REPTO; IPR01397; Terpend Synth.C.
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61.2%; Score 2844; DB 10;
Best Local Similarity 62.3%; Pred. No. 4.1e-200;
Matches 546; Conservative 120; Mismatches 183;
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Q38710; Q38710; Q38710; Created)
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ables grandis (Carad fir).
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Ables.
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MEDLINE=98284004; PubMed=9618485;
MEDLINE=98284004; Crock J., Jetter R.;
Bohlmann J., Crock J., Jetter R.;
Trepenoid-based defenses in conifers: cDNA cloning, characterization, and functional expression of wound-inducible (E)-alpha-bisabolene synthase from grand fir (Abies grandis).";
Proc. Natl. Acad. Sci. U.S.A. 95:6756-6761(1998).
EMBL; AF006195; AAC24192.1; -.
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   PPCFAGQTQ1GVTDNLNLYRCSQVCFPGEK1MBEAKTFTTNHLQNALAKNNAFDKWAVKK
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Abies.
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Best Local Similarity 49.5%; Pred. No. 1.6e-146;
Matches 397; Conservative 159; Mismatches 227; Indels 19;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 25, Last annotation update)
61-Supha-blasbolene synthase.
Abies grandis (Grand fir).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; NCBL_TaxID=46611;
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR005630; Terpene_synth_C.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR001906; Terp_cyc_foroid.
InterPro; IPR001906; Terp_synth-like.
Pfam; PF01397; Terpene_synth, 2.
Pfam; PF01395; Terpene_synth, C; 1.
SEQUENCE 817 AA; 93749 MW; 95FB06DBC
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MEDLINE=21297238; PubMed=11404343;

Trapp S.C., Croteau R.B.;

Trapp S.C., Croteau R.B.;

Genomic organization of plant terpene synthases and molecular evolutionary implications.;

Genetics 158:811-832(2001).

Genetics 158:811-832(2001).

GO; GO:0016829; F:lyase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IRR001330; Prenyltrans.
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                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Abietadiene synthase (Fragment).
Abies grandis (Grand fir).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; NOBI_TaxID=46611;
                                                                                          873
                                                                                                                  'Match 60.8%; Score 2822; DB 10; Local Similarity 62.8%; Pred. No. 1.6e-198; es 538; Conservative 121; Mismatches 172;
                                                                                    NTARVMOLFYMYRDGFGIS-DKEMKDHVSRTLFDPVA
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                                                                                                                                                                                                                      LPYHLPFISQIHQKRQKKLQKIPLAVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGSF
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                                                                                                                                                     ery Match 45.3%; Score 2103.5; DB 10; Length st Local Similarity 49.3%; Pred. No. 1e-145; tches 395; Conservative 160; Mismatches 228; Indels
                                                                                                                            816 AA; 93518 MW; 684FD528D1EC67E4 CRC64;
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR0085630; Terpene synth.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008930; Terp_cyc_foroid.
InterPro; IPR001906; Terp_synth-like.
Pfam; PF03197; Terpene_synth; 2.
Pfam; PF031936; Terpene_synth; 2.
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SEQUENCE 816 AA; 93518 MW; 684FD528D
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MEDLINE=99435880; PubMed=10504563;
Richman A.S., Gijzen M., Starratt A.N., Yang Z., Brandle J.B.;
Richman A.S., Gijzen M., Starratt A.N., Yang Z., Brandle J.B.;
Richman A.S., Gijzen M., Starratt A.N., Yang Z., Brandle J.B.;
Interprese synthesis in Stevia rebandiana: recruitment and up-
regulation of key enzymes from the gibberellin biosynthetic pathway.";
Interprese plant J. 19:411-421(1999).
REMBL; AR044545; AAB87091.1;
REMBL; AR04455; PRB80991.1;
REMBC; GO:000152; P:lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
RICHEPRO; IPR0015630; Terpene synth C.
RICHEPRO; IPR001906; Terp synth.
RICHEPRO; IPR001906; Terp synth-like.
RICHEPRO; IPR001906; Terp synth-like.
Refam; PR01397; Terpene synth, 1.
Refam; PR01397; Terpene synth, 1.
Refam; PR01397; Terpene synth, 2.
REQUENCE 787 AA; 90445 MW; 224575732606DCAI CRC64;
                                                                                                                                                                                       MGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRVL 191
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GYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALATVVLNSI-FPTGELLPD
                                                                SPFRKGWEDYLLGYYEEAEWLAAEYVPTLDEYIKNGITSIGQRILLLSGVLIMDGQLLSQ
                                                                                                         XILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSSVQCYMRENPECTEBEAL
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224575732606DCA1 CRC64;
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Last annotation update)
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772 IKECLIEPL 780
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                                                                                                                                                                             MEDLINE-98284004; PubMed=9618485;
MEDLINE-98284004; PubMed=9618485;
Bohlmann J., Crock J., Jetter R., Croteau R.;
"Terpenoid-based defenses in conifers: cDNA cloning, characterization, and functional expression of wound-inducible (E)-alpha-bisabolene synthase from grand fir (Abies grandis).";
Proc. Natl. Acad. Sci. U.S.A. 95:6756-6761(1998).
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                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-0CT-2003 (TrEMBLrel. 15, Last annotation update)
8-alpha-bisabolene synthase (Fragment).
Abies grandis (Grand fir).
8-alpha-bisabolene synthase (Sregment).
Abies Juidiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
NCBI_TAXID-46611;
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Matches 391; Conservative 158; Mismatches 221; Indels
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GO: 60:0008152; P:metabolism; IEA.
GO: GO: 0008152; P:metabolism; IEA.
InterPro: IPR008549; Terpene synth.
InterPro: IPR008949; Terpenoid synth.
InterPro: IPR008930; Terp_cyc_foroid.
InterPro: IPR001906; Terp_synth.like.
Pfam; PF03936; Terpene synth; 1.
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            PRELIMINARY;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Plantaginaceae; Gratioleae; Scoparia.
NCBI_TaxID=107240;
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                                                                                  VQKGVEFVRKHMBEMKDEADNHRPSGFEVVFPAMLDEAKSLGLDLPYHLPFISQIHQKRQ
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LTAHYQPS-----PSSSPPNQPFKFLKSNREHVEFNRILQCHAVSRRTKDYKEVQSG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamilds; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIAYAKTSCLAVILDDLYD-THGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYN
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                                              SFLSSPASTACVFWHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGID
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                LDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDG
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llarity 36.6%; Pred. No. 1.2e-92;
Conservative 141; Mismatches 275; Indels 125;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Copalyl diphosphate synthase.
CPS.
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Eukaryota, Viridiplantae,
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                                                                                                                                                       Query Match
29.2%; Score 1354.5; DB 10; Length 827;
Best Local Similarity 34.7%; Pred. No. 1.2e-90;
Matches 307; Conservative 154; Mismatches 284; Indels 139;
       SEQUENCE FROM N.A.

A SITCHILHAWORN W., Sankawa U.;
SICHILHAWORN W., Sankawa U.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RMBL; AB046689; BAB03594.1; -..
RMBL; AB046689; Pentabolism; IEA.
GO; GO:0001822; Pentabolism; IEA.
InterPro; IPR008949; Perpend Synth.
InterPro; IPR008930; Terpend Synth.
InterPro; IPR001906; Terp_Gyc_coroid.
InterPro; IPR001906; Terp_Gyc_coroid.
InterPro; IPR001906; Terp_Synth-like.
Pfam; Pf01936; Terpend—Synth.1:
Rem; Pf01936; Terpend—Synth.1:
Rem; Pf01936; Terpend—Synth.1:
SEQUENCE 827 AA; 93635 MW; FD94A6C281F9F382 CRC64;
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SItthithaworn W., Sankawa U.;

Sitthithaworn W., Sankawa U.;

"Copallyd liphosphate synthase from Croton sublyratus.";

"Copallyd liphosphate synthase from Croton sublyratus.";

EMBL, AB042424; BAA95612.1; -.

GO; GO:0016829; F:lyase activity; IEA.

GO; GO:0016829; F:lyase activity; IEA.

GO; GO:0016829; F:rpene synth.C.

InterPro; IPR006830; Terpene synth.C.

InterPro; IPR008930; Terpene synth.

InterPro; IPR001906; Terpene synth.

InterPro; IPR001906; Terpene synth.

InterPro; Terpene synth.

InterPro; Terpene synth.

InterPro; Terpene synth.

IPR01906; Terpene synth.

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VNGGCMTDVGGILSAQIESNMQELAKLVPTKSSS---GDLDSDTKQ-
                                                                                                                                                      | : | | : | | : | | - - - - - - CNPGSINFHIAKVLFBRV
                                                                                                           CVRRLLFNTARVMQLFY - - MYRDGFGISDKEMKDHVSRTLFDPV
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Last annotation update)
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(TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
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                                                                                                                                                                       FLHLVSLTGRL-----INDIKTYQAERNRGELVSSVQCYMRENPECTEERALSH 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=COLUMBIA;
MEDLINE=95086384; PubMed=7994182;
Sun T.D., Kamiya Y.;
Sun T.D. Asabidopsis Gal locus encodes the cyclase ent-kaurene synthetase
A of gibberellin biosynthesis.";
Plant Cell 6:1509-1518(1994).
                                                                                                                                      LTNWEKDGD------KHRGKAELIVKTINLT----TGPWVSEELL---NCNSK
                                                                                                                                                                                                                                         SKRELLLAYYISAASIFEPEKSKERLAWAKTSILLQTIDAYFHTNNSIEERKDF---VHQ
                                                                         WDISVL------DSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGL
                                                                                        FINELLLPHLEWIRGENGREDKAGTCRNYTWN-LKRCPLDALVAHGTDISHSLRHAWEIG
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SEQUENCE FROM N.A.
SEQUENCE COlumbia,
de la Bastide M., Gnoj L., Habermann K., Huang E.N., Gottesman T.,
Kaplan N., Lodhi M., Jensen K., Hameed A., Schutz K., Martienssen R.,
Dedhia N., Parnell L.D., McCombie W.R.,
"Arabidosis thaliana BAC T5J8 from chromosome IV, short arm.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
YGGDDDVWIGKVLYRMPFVNNNEYLELAKFDYNSCQALHRAEWDNFQKWYDECNLGDFGV
                         TRORPVEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRR
                                                                                                                                                                                                  738 YEKLFQLSNYLYHQLGHFNKNKVDDKKKY-------TTPE-----TTPE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ENT-KAURENE synthetase.
GA1 OR TS-38.9 OR AT4G02780.
Arabidopsis thaliana (Mouse-ear cress).
Rubaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea; Arabidopsis.
NBI TAXID=3702;
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U11034; AAA53632.1; -.
EMBL; AC04044; AAD15334.1; -.
EMBL; AL16495; CAB77763.1; -.
PIK; D85035; D85035.
GO; GO:0016829; F:lyase activity; IEA.
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SKVLFERV 828
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SEQUENCE FROM N.A.
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EWSAAKYVPTFNEYVENAKVSIALATVVL---NSI--FFTGELLPDYILQQVDLRSKFLH 759
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InterPro; IPR005630; Terpene synth C.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008930; Terp_cyc_toroid.
InterPro; IPR001906; Terp_synth-like.
Pfam; PF01397; Terpene_synth; 1.
Pfam; PF0336; Terpene_synth C; 1.
SEQUENCE 802 AA; 93013 MW; B2815AB0C06414F6 CRC64;
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53 PPTQEYSDVLQSGVPVIKWQQPVEDDIESETT--AHVLISKEIEERVNR-----IKS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 MLSSMDDGDISISAYDTAWYALIPRVLDGVKTPLFPSSLEWIAQNQLPDGSWGDSGIFSA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 KLQAPDGSFLKSPASTARAFMKTNNSNCFKYLBSVVSRFNGGVPNVYPVDLFEHIWAVDR 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POEERFVSRLNADYHPAVWK---DDFIDSLTSPNSHATSKSSVDETINKRIQTLVKEIQC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQF-GSNDVWLGKTVYKML 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDV--VDWQBIT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MFQSMGDGETNPSAYDTAWVARIPSI-DGSGAPQFPQTLQWILNNQLPDGSWGEECIFLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDT
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99063778; PubMed=9847116;
Smith M.W., Yamaguolhi S., Alt.-Ali T., Kamiya Y.;
"The first step of gibberellin biosynthesis in pumpkin is catalyzed k
at least two copalyl diphosphate synthases encoded by differentially
                                                                                                                                                                                                                                                                   Cucurbita maxima (Pumpkin) (Winter squash).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Cucurbitales, Cucurbitaceae, Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.5%; Score 1323.5; DB 10; Length 823; 36.8%; Pred. No. 2.2e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336; Terpene_synth_C; 1.
823 AA; 93946 MW; 3F367AAF474721F7 CRC64;
                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304; Conservative 148; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Physiol. 118:1411-1419(1998).

EMBL, AP049905; AAD04292.1; -.

EMBL, AP049905; AAD04292.1; -.

GO; GO:0001632; F: lyame activity; IEA.

GO; GO:0008152; P: metabolism; IEA.

InterPro; IPR008949; Terpenoid synth.

InterPro; IPR008949; Terpenoid synth.

InterPro; IPR001906; Terp cyc toroid.

InterPro; IPR001906; Terp synth-like.

Pfam; PF01397; Terpene_synth, 1.

EPONENGE SYNTH, 1.
                                                                                                                                                                                    (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                  Copalyl diphosphate synthase 1
                                                                                                                                              PRELIMINARY;
                         | : |:| : |
HPOYRLLSSVINNI
    KVSIALATVVLNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulated genes."
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3661;
                                                                                                                                                                                      01-MAY-1999
    723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISCLAVILDDLYDTHG---SLDDLXLFSEAVRRWDISVLDSVRDNQLXVCFLGLYNTVNG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGKDGLKEQGRDVLGYLRKVWEGLLASYTK---EAEWSAAKYVPTFN----EYVEN---A 722
                                      Lactuca sativa (Garden lettuce).
Bukaryocta; Vitidiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTLVDTISSFF--HSLKISNEHRREFVEEFRNISNSIHHAKYGKPWHGLMVALKGTLHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 799;
                                                                                                                                                                       Query Match 28.6%; Score 1326.5; DB 10; Lengt Best Local Similarity 40.8%; Pred. No. 1.3e-88; Matches 275; Conservative 126; Mismatches 224; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51940A6553B40BA5 CRC64;
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91865 MW; 5
  Copalyldiphosphate synthase Nol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            799 AA;
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NEKYLELAKLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPF 605
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                                                                                                                                                      DELLDKWIITKOLPGEVGYALDVPWFASLPRVETRYFIEQYGGENDIWIGKTLYRMFKVN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 RAKERLAWTKTAALVGAIESHF-KDANADQRRAFIQQFINFD--AIDQAYDTNAWRAGNV 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLKVCFLG----LYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVP 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 KTYQAER--NRGELVSSVQCYMRENPECTEBEALSHVYGIIDNALKELNWELANPASNAP 829
                                                                                                                                                                                                                                                        LGIDRYFKKEIKESLDYVYRYMDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDV 427
                                                                                                                                                                                                                                                                                                                                                                                                       428 LENFRDEKGDFFCFAGQTQIGVTDNLNLYRCS-QVCFPGEKIMEEAKTFTTNHLQNALAK 486
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                                                                                                                                                                                                                                                                                                     NNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQF-GSNDVWLGKTVYKMLYVS
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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K MEDLINE-95210929; PubMed=7696880;

A Meeley N.B., Briggs S.P., Crane V.C., Tossberg J.T., Schnable P.S.

A Meeley N.B., Briggs S.P., Crane V.C., Tossberg J.T., Schnable P.S.

T "Cloning and characterization of the maize An1 gene.";

Plant Cell 7:55-84(1995).

R EMBL; La7750; AAA73960.1; -.

R EMBL; La7750; AAA73960.1; -.

R GO; GO:0016829; F:1Vase activity; IEA.

R GO; GO:0016829; F:1Vase activity; IEA.

R GO; GO:0016829; F:Tepenoid synth C.

R InterPro; IPR008930; Terpenoid synth.

R InterPro; IPR008930; Terpenoid synth.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                         ---QLKVCFLG----LYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAK 710
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               YVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMF
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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"Cucurbita maxima mRNA for copalyl diphosphate synthase 1,
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28.4%; Score 1319; DB 10; Length
Best Local Similarity 36.8%; Pred. No. 4.8e-88;
Matches 303; Conservative 145; Mismatches 301; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                           Query Match 28.4%; Score 1318; DB 10; Length 823; Best Local Similarity 35.0%; Pred. No. 5.7e-88; Matches 302; Conservative 157; Mismatches 275; Indels 130;
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Pfam; PF01397; Terpene_synth; 1.
Pfam; PF03936; Terpene_synth_C; 1.
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RESULT 1
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DEFINITION
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KEYWORDS
SOURCE
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                    - nucleic search, using sw model
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dinkgo biloba (maidenhair tree)
Ginkgo biloba
Ginkgo biloba
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 2705)
Schepmann, H.G., Pang, J. and Matsuda, S.P.
Chepmann, H.G., Pang, J. and Matsuda, S.P.
Cloning and characterization of Ginkgo biloba levopimaradiene synthase which catalyzes the first committed step in ginkgolide REFERENCE AUTHORS TITLE

is the number of results predicted by chance to have a

Pred. No.

AF331704 2705 bp mRNA linear PLN 03-OCT-2001 Ginkgo biloba levopimaradiene synthase mRNA, complete cds. AF331704.1 GI:15865604

ALIGNMENTS

BD227676 Synthases AR240711 Sequence AR26986 Sequence AR38478 Sequence AR3842107 Sequence AR22107 Sequence AR2202107 Sequence AR266981 Sequence AR266981 Sequence AR266981 Sequence AR38473 Sequence AR366981 Sequence AR366981 Sequence AR36698 Sequence AR30309 Sequence AR230309 Sequence AR230309 Sequence AR230309 Sequence AR230309 Sequence AR23030 Sequence AR230309 Sequence AR230287 Sequence AR230287 Sequence AR230287 Sequence AR230287 Sequence AR230287 Sequence AR240705 Sequence AR38472 Sequence AR36598 Sequence AR36599 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence AR366980 Sequence Ginkgo bi Synthases Abies gra Pinus tae Picea abi Picea abi Sequence Synthases Abies gra Croton su Sequence Abies gra Pinus tae Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AR222137 & AF139205 A AF139205 A AF34330 B AF461460 B AR222146 S AR339206 A AB042424 C AR222116 S BD227672 & SUMMARIES AR266966
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AR347320 В Length Query Match 221.1 200.1 190.0 118.6 118.6 118.6 118.5 118.5 118.5 118.5 2241 10078 1 450.4 450.4 429.6 425 417.2 Result No.

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Best Local Similarity 100.0%; Score 2241; DB 8; Length 2705;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2241; Conservative 0; Mismatches 0; Indels 0;
                                                                                          University,
                       (2), 263-269 (2001)
                                                                                          Rice
           biosynthesis
Arch. Biochem. Biophys. 392 (2), 263-31381393
11488601
2 (bases 1 to 2705)
Schepmann, H.G. and Matsuda, S.P.T.
Direct Submission
Submitted (21-DEC-2000) Chemistry, Ristreet, Houston, TX 77005, USA
Location/Qualifiers
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CC12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/
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48.1%; Score 1078; DB 6;
Best Local Similarity 68.8%; Pred. No. 1.5e-309;
Matches 1544; Conservative 0; Mismatches 685;
                                                                                                                                                Location/Qualifiers (3). (2606).
Location/Qualifiers

    .2861
    /organism="Abies grandis"
/mol_type="genomic DNA"
/db_xref="taxon:46611"

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UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES
OS Abies grandis (giant fir)
N JP 200252666-A/28
PD 20-AUG-2002
PF 17-SEP-1999 JP 2000574228
PR 17-SEP-1999 US 60/15052
PR 18-528-1999 US 60/15052
PR 19-528-1999 US 60/15052
PR 19-528-1999 US FOUNDEDLE RANNA, JOSEPH P NOEL, COURTNEY M PI
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Abies.
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9y 1111 GCTTGTAGAATGCCTATGCCAAAACTTCCTGCGAGTTATTCTAGACACTCTTTAC 1500 1815 AAGTCCAAGAGAGTTATACAAAACTTCCATCATTCAACGAGAGAGA	RESULT 4 AR266986 LOCUS AR266986 AR266986 LOCUS AR266986 AR266986 AR266986 AR266986 AR266986 AR266986 AR266986 AR266986 AR266986 AR266986 AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 ARSION AR266986 AR2669
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 /organism="unknown"
 /mol_type="genomic DNA" Query Match Best Local Similarity 68.8%; Matches 1544; Conservative 8 6 8 6 8 6 6 8 6 8 6 8 6 8 6 8 6 8 6 8 & 8 6 6 6 6 6 g

TTACAGCAAGTAGACCTTGGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTA GGTATCATCGACAACGCACTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGCGAGCAAT TATCTTCGAAAAGTATGGGAGGGTTGCTCGCATCGTATACCAAAAAAGCCGAATGGTCG GCAGCAAAGTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCATAGCA CITGGGACAGIGGIAGIAAACICAAICITITICACIGGAGAAITACITCCIGAITACAIT AACACAGTGAATGGATTTGGAAAAGATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGC GCTIGTAGAATIGCCTAIGCCAAGACTICTIGCCTCGCAGTIATICTAGACGATCTITAC ATCTCTGTGCTGGATAGGCTTCGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTAC GGTGTGACCGATAATCTTTATAGATGTTCACAAGTATGTTTTCCGGGAGAAAAG

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                       AACACAGTGAATGGATTTGGAAAAAAATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGC
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                                                                                                                                                                                                                                                                                                                                                          Score 1078; DB 6; Length 2861;
Pred. No. 1.5e-309;
0; Mismatches 685; Indels 15;
                                                                                                                                                                             Unknown.
Unclassified.
Unclassified.
Chapsell, J., Manna, K.R., Noel, J.P. and Starks, C.M. Synthases
Patent: US 645762-A 55 11-NOV-2003;
Location/Qualifiers
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Sequence 55 from patent US 6645762.
AR429884.1 GI:40190282
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 68.8%;
Matches 1544; Conservative
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2232 CTCTCCAAAATTGATCGCGAATCTAGATTCTTCAACTCATGGGCTTAACAGGGCGTTTG
                                                                  AAATATTIGGAGCTGGCCAAATTGGACTTCAATATGGTGCGCGGGCCTTACACCAAAGGAG
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                             CAGCGGCCTGTGGAAATGTATTTCTCAGTGGCGGTTAGTATGTTTGAGCCAGAATTCGCT
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LYLRWGRGSNKIIACVGEGGATSVPYQSAEKNDSLSSSTLVKREFPPGFWKDDLIDSL
TSSHKKAASDEKRIETLISEIKNMFPCMGYGETHPSBAYDTMWARIPAVDRIPHPP
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AGKMEDDEADSTRPROGFBEIVPPAMLKERKILGIDLPYDLPFLKQIIEKREAKLKRIPTD
VLYALPTTLLYSLEGLQEIVDWQKIMKLQSKDGSFLSSPASTAAVFMRTGNKCLDFL Abies grandis abietadiene synthase (ac22) mRNA, complete cds. U50768.1 GI:1477583 2465 2160 2217 2526 Argciaggiciarigan arctarcacaticaratica artha a garciar communication of the communicatio 2100 Abies grandis
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NFVLKKFGNHVPCHYPLDLFRRLMAVDTVBRLGIDRHFKBBIKBALDYVYSHWDERGI GWARENPVPDIDDTAMGIRILRIHGYNVSSDVLKTFRDENGREFCFLGQTQRGYTDML NWRCSHYSEPGETIMERAKLCTERYRINALENDAFDKWAFKKNIRGEVEYALKYFW HKSMPRLEARGYIBYNYGPDDWIJCKTVYMPYISNBKYLELAKLDFRKYQSIHGTELQ DLRRWWKSSGFTDLNFTRERVTEIYFSPASFIFEPEFSKCREVYTKTSNFTVILDDLY DAHGSLDDLKLFTESVKRWDLSLVDQMPQQMKTCFVGFYNTFNDIAKEGRERQGEDDL GYLQWVWKVQLEAYTKKAEWSEAKYVPSFNBY1 ENASVSIALGTVVLISALFTGEVLT DEVLSKIDRESRFLQLMGLTGRLVNDTKTYQAERGQGEVASAIQCYMKOHPKISEREA LQHYXSVMENALEELNREFVNNKIPDIYKRLVFETARIMQLFYMQGDGLTLSHDMEIK EHVKOCLFQPVA" 1037 1097 1157 1214 4. 240 120 180 840 437 300 420 900 099 720 780 497 557 617 677 360 737 797 480 857 540 917 977 900 9 GCAAGAATTCCGTCAATTGACGGCTCTGGTGCACCCCAATTTCCCCAAAACGCTTCAATGG AAAATCTTAGGCTTGGATCTGCCTTAGGATTTGCCATTCCTGAAACAAATCATCGAAAAG ATGTTTCAGTCCATGGGCGACGGTGAAACGAATCCATCTGCATATGATACAGCTTGGGTG ATGITIAGATGTATGGGCTATGGCGAAACGAATCCCTCTGCATATGACACTGCTTGGGTA GACAGAGTTTTAAACACTCTCGCCTGCCTCCTCACTCTCAAAATATGGAATAAGGGCGAC GCTGATAGTCATAGGCCAAGTGGATTTGAAATAGTATTTCCTGCAATGCTAAAGGGT ATTCTGAACAATCAACTGCCAGATGGCTCGTGAGGAGTGCATTTTTCTGGCGTAT GACAGAATACTGGCTACACTTGCATGTATTATTACCCTTACCCTCTGGCGTACTGGGGAG ATTCAAGTGCAGAAAGGGGTTGAGTTTGTGAAAAACACATGGAAGAAATGAAGGACGAA GCTGACAATCACAGGCCAAGTGGATTCGAGGTCGTGTTTCCTGCAATGTTAGATGAAGCA CGCCAGAAAAAGCTTCAAAAGATTCCCCTCAAATGTTCTTCATAACCATCAGACGGCGTTG CTCTACTCTCTGGAGGGTTTGCAAGATGTGGTGGACTGGCAAGAGATCACAAATCTTCAA TCAAGAGGGATCATTTTAAGCTCCCTGCATCTACTGCTTGTGTCTTCATGCACACT CAAAACAAACGATGCCTCCACTTTCTCAACTTCGTGCTCAGCAAATTTGGCGACTACGTT GGGAACAAAAAGTGCTTGGATTTCTTGAACTTTGTCTTGAAGAATTCGGAAACCATGTG CCTTGTCACTATCCGCTTGATCTATTTGAACGTTTGTGGGCGGTTGATACAGTTGAGCGG TTGGGAATCGATCGCTATTTCAAGAAAGAAATCAAAGAATCTCTGGATTACGTTTATAGG CTAGGTATCGATCGTCATTTCAAAGAGGATCAAGGAAGCATTGGATTATGTTTACAGC CATTGGGA----CGAAAGAGGCATTGGATGGGCGAGAGAATCCTGTTCCTGATATTGAT GACACTGCCATGGGTCTTAGAATCCTGAGACTTCATGGATACAATGTATCTTCAGATGTT <u> ATTCTTCAAAATCAGTTGAAAGATGGGTCTTGGGGTGGAAGGATTCTTCTTTGGCATAT</u> CCTTGCCATTACCCACTTGATCTATTTGAACGCCTCTGGGCTGTCGATACAGTTGAACGC TACTGGGACGCCGAAAGAGGCGTGGGATGGATGCAATCCTATTCCTGATGTCGAT Gaps 15; Length 2861; Indels Ouery Match

48.1%; Score 1078; DB 8;
Best Local Similarity 68.8%; Pred. No. 1.5e-309;
Matches 1544; Conservative 0; Mismatches 685; 1038 1098 1158 378 61 438 121 498 181 301 361 738 421 798 481 858 541 918 601 661 721 781 841 셤 ઠે g δ g ठे 음 중 음 **68686** 8 8 8 8 8 8 8 셤

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UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE
BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN
SERVICES
                                                                                  2041 GGTATCATCGACACGCACTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGCGAGCAAT
                                                                                                  2101 GCCCCATTGTGTGAGAAGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTAT
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                                   CAGTGCTACATGAGGGAAAATCCGGAGTGCACAGAAGAAGAAGCTCTAAGTCATGTTTAT
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Spermatophyta, Coniferopsida, Coniferoses; Jl (bases 1 to 2424)
Chappell, Manna, K.R., Noel, J.P. and Starks, C.M.
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AAGAGTGTCTCATTGAACGGCTGCC 2343 ind Starks, C.M. des ΑN

2424; 21; Gaps 6;	ACGCTCTGT 90	CAGATGGCTCG 150		TTGAGTTTGTG 270 	CAAGTGGATIC 327 	ATCTICCITAT 387 GACTICCTAC 493	AAAAGATTCCC 447 CAAAACTTTCA 553	GTTTGCAAGAT 507 GAATACAAGAT 613		TCTTAAGCTCA 673		TITGALCIATIT 687			AGAGGAATTGGG 910 CTTAGAATCCTG 867		GACGAGAAAGGA 927 	CTTAACCTTTAT 987		AAAAGCTTCGCT 1150 TGGGCTGTCAAG 1107
Query Match 32.3%; Score 723.4; DB 6; Length 2 Best Local Similarity 59.8%; Pred. No. 8.7e-204; Marches 1327; Conservative 0; Mismatches 871; Indels	¥=¥	GCACCCCAATTTCCCCAAACGCTTCAATGGATTCTGAACAATCAACTGCCAGATGGCTCG	regecterantiticecementitions sont instrumentations record reger reger regections and the sont reger re	CICACICIAAAATAGAATAAGGGCGACATICAAGTGCAGAAAGGGGTIGAGTITGIG 	AGADADACAGTIGGAAGAAATGAAGGACGAAGCTGACAATCACAGGCCAAGTGGATTC AGAGCAATCTGGAACTAGTAAAGGATGAAACCGATCAAGATAAGCTTGGTAACAGATTTT	GAGGTCGTGTTTCTGGAATGTTAGATGAAGCAAAAGCTTGGGATTGGATCTTCCTTAT 	CACCTCCCTTTCATCTCCCAAATCCACCAAAAGCGCCAGAAAAAGCTTCAAAAGGTTCCC	CTCAATGTTCTTCATAACCATCAGACGGCGTTGCTCTACTCTCTGGAGGGTTTGCAAGAT CTCAATGTTCTTCATAAACATTGTTGTTGTATTGTA	GIGGIGGACTGCAAGATCAAAATCTTCAATCAAGAGACGGATCATTTTAAGCTCC	ATAGTTGAATGGGAACGAATAATGGAAGTTCAAGTCAGGATGGGTCTTTCTT	CCIGCALCIACION CONTROL	AACTICGIGCICAGCAAATIIGGCGACIACGIICCTIGCCATIACCCACIIGAICIAIII	GAACGCCTCTGGGCTGTCGATACAGTTGAACGCTTGGGAATCGATCG	GAATCACAGATCTCTGGGTTACGTTTATAGGTACTGGGACGCCGAAAGAGGCGTGGGA	.phaitchaggaagctcttgattatgtttacaggcattggaacga .cocoss.cs.cs.cocoss.cc.cs.cc.cs.cc.cs.cc.cs.ca.cc.ca.cc.cs.cs.cs.cocoss.cs.cs.cc.cs.cc.cs.cc.cs.cs.cs.cs.cc.cs		agacticatggatacaigitaicticagatgtictggagaatticagagacgagaaagga 	GACTICITITICITITICCOGGICAAACGCAAATICGIGIGACCGATAATCTITAACTITITI	AAATTCATTTGCTCGACCGGTCAATTCAACAAAAATTGTAAGAAAAAAAA	
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734 AACAGTGTGATGATCAAGTTTGGAAATTTTGTTCCCTGCCTG		1048 ACAAATCATCTCAAAATGCTCTTGCCAAAACAACGCATTTGATAAGTGGGCTGTCAAG	1168 AGATTGGAGGAAGAAGTTACATAGAGCAATTTGGATCAAATGATCTGGCTGG	1288 TTCAATATGGTGCAGCCTTACACCAAAAGAGAGACTCAACATTGTCAGCTGGTGGAGA 1347	1408 GTGGCGGTTAGTATGGCCAGAATTCGCTGCTTGTAGAATTGCCTATGCCAAGACT 1467	1528 AAATTGTTCTCTGAAGGGTCCGAAGATGGGATATCTCTGTGCTGGATAGCGTTCGGGAT 1587	1648 GGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAAAAGTATGGGAGGCTTG 1707 1748 GCAGAGAAGAACAGGGGCGTGAATTGGTCAGCTTTTTCAGAAAGGGATTAT 1807 1708 CTCGCATCGTATACCAAAGAAGCCGAATGGTCGCGCAGCAAGTATCAAC 1767 1808 CTTCTGGGTTATTATGAAGAAGCTGAATGGTTAGCTGCTGAGTATGTGCCGACATTCAAC 1767 1808 CTTCTGGGTTATTATGAAGAAGCTGAATGGTTAGCTGCTGAGTATGTGCCTACGAC 1867
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CTTGCCAAAAACAACGCATTTGATAAGTGGGCTGTCAAG 1107
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1. .2424
/organism="unknown"
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                          GATTCGGGGTTGCCACTATTCACCTTCGCTGGAGGCGCTGGAATTCTACTTCTTA
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GAATCGGGATTCAATGATCTTACATTCACCGGCCAGCGGCCTGTGGAAATGTATTTCTCA
                                                                                     GTGGCGGTTAGTATGTTTGAGCCAGAATTCGCTGCTTGTAGAATTGCCTATGCCAAGACT
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	Description	Aaa38937 Grand fir	Aax08654 Grand Fir	Aaa38932 Grand fir	Aaf73382 Grand fir	Aax87530 E-alpha-b	Aax87529 Grand fir	Aax87531 E-alpha-b	Aax87504 Grand fir	Aat97447 Pacific y	Aaa38931 Yew taxad	Aaf73412 Grand fir	Aaf73421 Grand fir	Aax08663 Grand Fir	Aaf73391 Grand fir	Aaa38933 Grand fir	Aax87532 Delta-sel	Aax87534 Delta-sel	Aax87533 Delta-sel	Aax87505 Grand fir	Aax08643 Myrcene s	Aaa38927 Grand fir	Aaf73371 Grand fir	Aax87513 Grand fir
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ALIGNMENTS

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RESULT 1

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Synthame; protein co-ordinate data; active mite; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthame; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antitumour; steroid hormone; algnal transduction pathway; blle acid; affinity purification; photoreceptor; enzymatic synthemis; nutrient supplement; immunological reagent; dm. Grand fir abietadiene synthase DNA sequence SEQ ID NO:55. Starks CM; (KENT) UNIV KENTUCKY RES DEPT. (SALK) SALK INST BIOLOGICAL STUDIES. Noel JP, 98US-0100993P. 99US-0130628P. 99US-0150262P. 99WO-US021419 25-AUG-2000 (first entry) WO200017327-A2 Abies grandis. 18-SEP-1998; 22-APR-1999; 23-AUG-1999; 17-SEP-1999; 30-MAR-2000.

Chappell J, Manna KR, WPI; 2000-292839/25. P-PSDB; AAY90858. Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.

Disclosure; Page 439-443; 450pp; English.

The present invention describes an isolated terpene synthase (I) comprising a region with at least 20% identity to region 265-535 of a 548

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carbon atoms (alphaC) that have interatomic distances, between each cherwon atoms (alphaC) that have interatomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom) within tabulated ranges, and have an ordered carangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and contained arrangements (tables given in the specification). (I), and contained arrangements (tables given in the specification). (I), and contained a signal transductor a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, antitumour agents, components of signal transduction pathways, precursors of steroid components of signal transduction pathways, precursors of steroid components of signal transduction pathways, precursors of steroid components of signal transduction pathways, precursors of steroid components of such a sphetoreceptors and as co-factor side chains. Components of signal little or no catalytic activity (and nucleic acids convanted propersors) as nutrient supplements; for affinity purification of septencides, as nutrient supplements; for affinity purification of septences of products or nucleic acids for monitoring expression of terpene synthases may produce novel terpene convaluation of products. Analssis and Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi to Anaysossi 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 68.8%; Pred. No. 0;
Matches 1544; Conservative 0; Mismatches 685; Indels
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Nucleotide sequences encoding mycrehe synthase, limonene synthase and pinene synthase from Grand fir may be incorporated into any organism (e.g. inteat plant, animal, microbe), or derived cell culture that produces geranyl diphosphate for the production of the aforementioned enzymes or their products. The sequences when expressed in transfected cells may also be used for the production of modification of flavour and aroma properties, improvement of defense capability, and the alteration of other ecological interactions mediated by mycrene, limonene, pinene, of other ecological interactions mediated by mycrene, limonene, pinene, of plant seeds for the extraction of oil or meal. cDNAs encoding myrcene synthase, pinene synthase and limonene synthase from Grand Fir were sequences of different plant synthase enzymes, four conserved sequences of different plant synthase enzymes, four conserved sequences were identified for construction of four degenerate primers (AAX08646.

49). One of these primers (AAX08648) was an antisense primer and used for primer the orbor three senses primers. Only a combination of primers (AAX08649 generated a PCR product which was 110 base pairs in CCC transform E.coll XII-Blue cells and the inserts were sequenced. Four CCC transform E.coll XII-Blue cells and the inserts were sequenced. Four concern a Grand Fir CDNA library. One of these clones is the myrcene conserved in a synthase sequenced general conserved in the conserved conserved in the conserved conserved in the modified are sequenced in the conserved in the modified are conserved in the conserved in the modified are conserved to screen a Grand Fir CDNA library. One of these clones is the myrcene conserved in the conserved conserved in the conserved conserved in the conserved conserved in the conserved conserved in the conserved conserved in the conserved conserved in the conserved conserved in the conserved conserved conserved conserved conserved conserved conserved conserved conserved conserved conserved conserved conserved conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.3%; Score 723.4; DB 2; Length 2424; Best Local Similarity 59.8%; Pred. No. 4.1e-214; Matches 1327; Conservative 0; Mismatches 871; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2424 BP; 730 A; 472 C; 575 G; 647 T; 0 U; 0 Other;
      Example 1; Page 86-90; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               described in AAX08654-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2526 ATGCAAGGGATGGTTTGACACTATCACATGATATGGAAATTAAAGAGCATGTCAAAAT 2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycrene synthase; limonene synthase; pinene synthase; flavour;
monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene.
                                     2172 TIGGGAACAGICGTICTCATIAGIGCTCTTTTCACTGGGGAGGITCTIACAGAIGAAGIA
                                                                                                                                                                                          2232 CICICCAMATICATCGCGAATCIAGATITCITCAACICATGGGCTIAACAGGGCGTITG
                                                                                                                                                                                                                                                                                                        2041 GGTATCATCGACAAGGACTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGCGAGCAAT
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                                                                                                                               1861 TTACAGCAAGTAGACCTTCGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTA
                                                                                                                                                                                                                                                                                                                                                                                                  CAGTGCTACATGAGGGAAAATCCGGAGTGCACAGAGGAAGAAGCTCTAAGTCATGTTTAT
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2. .2350
/*tag= a /product= "Potential diterpene cyclase"
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22-APR-1999;
23-AUG-1999;
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                                                                                                                                                                                                                                                                               2047
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                                                                                                             TTTTCAC----TGGAGAATTACTTCCTGATTACATTTTACAGCAAGTAGACCTTCGGTCC
GAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCAATC
                                                     GGTATCTCTGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTTTCGATCCTGTGGC
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INST BIOLOGICAL STUDIES
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The present invention describes an isolated terpene synthase (1)

comprising a region with at least 20% identity to region 265-535 of a 548

amino acid (aa) sequence (1a), given in AAY99031. (1) contains nine alpha
carbon atoms (alphaC) that have interatomic distances, between each
carbon atoms (alphaC) that have interatomic distances, between each
cother, within tabulated ranges, have a centre point (within a sphere of
cardius 2.3 Angercom) within tabulated ranges, and have an ordered
arrangement of R groups (defining as side chains), excluding specific
carbulated arrangements (tables given in the specification). (1), and
cother, acylic, optionally hydroxylated), useful e.g. as fragrances,
flavours, pheromones, defensive agents, pigments, antitumour agents,
components of signal transduction pathways, precursors of steroids
components of signal transduction pathways, precursors of steroid
components of signal transduction pathways, precursors of steroid
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components of signal transduction from the analysis of products formed by
controling them) are used as controls in the analysis of products formed by
controling expression of terpene synthases or inheritance of the gene in
plant breeding programs. The new synthases may produce novel terpene
products. AAA38910 to AAA38938 and AAX90831 to AAA38911 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38931 to AAA38933 and AAX90831 to AAA38933 and AAX90833 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 to AAA38933 t
Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
                                                                                                                                                                              Disclosure; Page 414-418; 450pp; English
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Sequence 2424 BP; 730 A; 472 C; 575 G; 647 T; 0 U; 0 Other;

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447 91 GCACCCCAATTTCCCCCAAACGCTTCAATGGATTCTGAACAATCAACTGCCAGATGGCTCG 150 253 CTCACTCTCAAAATATGGAATAAGGGCGACATTCAAGTGCAGAAAGGGGTTGAGTTTGTG 270 crigingericerraanidaaacerredeaacineeaacineaacacacaaarridaarricara 373 AGAAAACACATGGAAGAAATGAAGGACGAAGCTGACAATCACAG---GCCAAGTGGATTC 327 374 AAGAGCAATCTGGAACTAGTAAAGGATGAAACCGATCAAGATAGCTTGGTAACAGACTTT 433 GAGGTCGTGTTTCCTGCAATGTTAGATGAAGCAAAAAGCTTGGGATTGGATCTTCCTTAT 387 GAGATCATATITICCTITCTCTGTTAAGAGGTCAATCTCTGCGCCTCGGACTTCCCTAC 493 GACCTGCCTTATATACATCTGTTGCAGACTAAACGGCAGGAAAGATTAGCAAAACTTTCA 553 448 CTCAATGTTCTTCATAACCATCAGACGGCGTTGCTCTACTCTCTGGAGGGTTTGCAAGAT 507 554 AGGGAGGAAATTTATGCGGTTCCGTCGCCATTGTTGTTTCTTTAGAGGGAATACAAGAT 613 GTGGTGGACTGGCAAGAGATCACAAATCTTCAATCAAGAGACGGATCATTTTTAAGCTCC 567 cerecerreracide entre de la contra del la contra della co 31 AATCCATCTGCATATGATACAGCTTGGGTGGCAAGAATTCCGTCAATTGACGGCTCTGGT 90 194 CGCCCGCAATTTCCCCAAACAGTTGACTGGATTTTGAAAAACCAGTTAAAAGATGGTTCA CACCTCCCTTTCATCTCCCCAAATCCACCAAAAGCGCCAGAAAAAGCTTCAAAAGATTCCC Pred. No. 4.1e-214; 0; Mismatches 871; Indels 21; Gaps 32.3%; Score 723.4; DB 3; Length 2424; 59.8%; Pred. No. 4.1e-214; Best Local Similarity 59.8 Matches 1327; Conservative 151 434 254 211 314 271 328 388 494 508 268 674 Query Match පු d 셤 셤 쉽 셤 ઠે g ઠે ò ò Š ò

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È	628 AACTICGIG	AACTICGIGCICAGCAAAIITGGCGACIACGTICCTIGCCATIACCCACTIGAICIAITI 687
qq	734 AACAGTGTG	7
è	688 GAACGCCTC	GAACGCCTCTGGGCTGTCGATACAGTTGAACGCTTGGGAATCGATCG
д	794 GAACGCCTG	rrdarceragaraararreracecrregaarcraragacacrrrgaaag 853
È	48	0
d d	854 GAAATCAAG	GAAGCICTTGATTATGTTTACAGGCATTGGAACGAAAGAGAATTGGG 910
à	808 TGGGCAAGA	TGGGCAAGATGCAATCCTATTCCTGATGTCGATGACACTGCCATGGGTCTTAGAATCCTG 867
Ор	911 TGGGGCAGA	CTAAATCCCATAGCAGATCTTGAGACCACTGCTTTGGGATTTCGATTGCTT 970
È	868 AGACTICAT	AGACTICATGGATACAANGTATCTTCAGATGTTCTGGAGAATTTTCAGAGACGAGAAAGA 927
qq	971 CGCTGCAT	AGGIACAAIGIAICTCCAGCCATTTTGACAACTTCAAAGAIGCCAAIGGG 1030
ò	928 GACTTCTTT	GACTICTITIGCTTIGCCGGTCAAAGGCAATIGGIGGACGATAATCTTAACCTTIAT 987
οp	1031 AAATTCATT	П
È	988 AGATGTTCA	AGATGTTCACAAGTATGTTTCCGGGAGAAAGATAATGGAAGAGAGAG
QQ	1091 AGAGCTTCC	cacregearticecegagaaaaartertaargaageraaaagrieger 1150
È	1048 ACAAATCAT	CAAATCATCTCCCAAAATGCTCTTGCCAAAACGCATTTGATAAGTGGGCTGTCAAG 1107
q	1151 ACTAAATAT	TIGAGAGAAGCTCTTGAGAAAAGTGAGACTTCCAGTGCATGGAACAACAAA 1210
ò	1108 AAGGATCTT	AAGGATCTTCCTGGAGAGGGGGGGTATGCTATAAAGTATCCGTGGCATAGAAGTATGCCA 1167
đ	1211 CAAAACCTG	AGCCAAGAGATCAAATACGCGCTGAAGACTTCTTGGCATGCCAGTGTTCCG 1270
È	1168 AGATTGGAG	AGATTGGAGGCAGAGAGTTACATAGAGCAATTTGGATCAAATGATGTCTGGCTGG
ą	1271 AGAGTGGAA	GCAAAGAGATACTGTCAAGTGTATGCCCCAGATTATGCACGCATAGCAAAA 1330
È	1228 ACTGTGTAT	AAGATGCTATATGTGAGCAACGAAAATATTTGGAGCTGGCCAAATTGGAC 1287
셤	1331 TGCGTTTAC	TGCGTTTACAAGCTACCCTACGTGAACAATGAAAGTTTTTAGAGCTGGGAAAATTAGAT 1390
ò	1288 TTCAATATG	GIGCAGGCCTTACACCAAAAGGAGACTCAACACATTGTCAGCTGGTGGAGA 1347
qq	1391 TTCAACATT	TTCAACATTATCCAGTCCATCCACCAAGAAGAATGAAGAATGTTACCAGCTGGTTTAGA 1450
ò	1348 GAATCGGGA	GAATCGGGATTCAATGATCTTACCTTCACCCGCCGGGGCCTGTGGAAATGTATTTCTCA 1407
qq	1451 GATTCGGG	rigccacraricacricecressassesecesessariciacritera 1510
ò	1408 GTGGCGGTT	GIGGGGGTTAGTATGTTTGAGCCAGAATTGCCTGTAGAATTGCCTATGCCAAGACT 1467
qq	1511 GTAGCGCCG	GGGACCTATGAACCCCAGTATGCCAAATGCAGGTTCCTCTTTACAAAAGTG 1570
ò	1468 TCTTGCCTC	TCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACCCACGGATCTCTGGATGATCTT 1527
οg	1571 GCATGCTTG	cagacrericricaacanarerardacacrrandaaacecradardaarig 1630
È	1528 AAATTGTTC	AAATTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTGGATAGCGTTCGGGAT 1587
q	1631 AAGCTATTC	actgaggcretgagaagarggaaccretecrtracagaaaccrecagae 1690
ò	1588 AATCAGTTG	AAAGTITGCITCCIAGGGCIGIACAACACAGATGGAATGGA
qq	1691 TATATG	argaaactargtraccaaarctarrargacargtrcacgaggrggcrrggaag
λŏ	1648 GGACTCAAG	GGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAAAGTATGGGAGGGCTTG 1707
셤	1748 GCAGAGAAG	GAACAGGGGGTGAATTGGTCAGCTTTTTCAGAAAGGGATGGGAGGATTAT 1807

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CTCGCATCGTATACCAAAGAAGCCGAATGGTCGGCAGCAAAGTATGTGCCGACATTCAAC
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                                                                                                                                                                                                                                                      GAGTACATAAAGAATGGAATCACATCTATCGGCCAACGTATACTTCTGTTGAGTGGAGTG
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The present invention provides the protein and coding sequences of monoterpene. Synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-limonene/(-)-alpha-pinene synthase, limonene synthase. myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants
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2178 2048 TATAAAGCTGAGAAGGCTCGTGGAGAATTGGCGTCCAGCATTGAATGTTACATGAAAGAC 2107 2168 GTGAAGGAACTGACAAGAGAGTTTCTGAAGCCCG---ACGACGTCCCATTCGCCTGCAAG 2224 AAGATGCTTTTCGAGGAGACAAGAGTGACGATGGTGATATTCAAGGATGGAGATGGATTC 2284 and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives GGTGTTTCCAAATTAGAAGTCAAAGATCATATCAAAGAGTGTCTCATTGAACGGCTGCC 2343 This is the sequence of a computer-generated nucleic acid coding for a grand fir (Abies grandis) B-alpha-bisabolene synthase polypeptide (see AAY06567) that has conservative amino acid substitutions relative to the native B-alpha-bisabolene synthase sequence given in AAY06562. B-alpha-bisabolene synthase is a wound- inducible enzyme capable of generating multiple sesquiterpenes, especially B-alpha-bisabolene, from farnesyl diphosphate. The invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, 88 1108 CATCCTGAATGTACAGAGGAAGAGGCTCTCGATCACATCTATAGCATTCTGGAGCCGGCG <u> AGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATATGTACAGAGATGGCTTT</u> **AATCCGGAGTGCACAGAAGAAGAAGCTCTAAGTCATGTTTATGGTATCATCGACAACGCA** grand fir; sesquiterpene synthase; disease resistance; fragrance; flavour; GGTATCTCTGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTTTCGATCCTGTGGC E-alpha-bisabolene synthase computer-generated nucleic acid sequence protein and Bohlman J, Jetter R, Steele CL; Grand fir (Abies grandis) sesquiterpene synthase genes products, useful for sesquiterpenoid production. (UNIW) UNIV WASHINGTON STATE RES FOUND Example 11; Page 95-98; 136pp; English.

1195 AGAGCTTCCCAGGTTGCCGGAGAAACAITCTTGATGAAGGTAAAAGGTTCGCT 1254		1108 AGGATCTTCCTGCAGAGGTGGAGTATGCTATAAGATATCCTGCAAAAAAAA	1375 AGAGTGGAAGGATACTGTCAAGTGTATCGCCCAGATTATGCACGCATAGCAAAA 1434 1228 ACTGTGTATAGATGCTATATGTGAGCAACGAAAAATATTTGGAGCTGGCCAAATTGGAC 1228 ACTGTGTATAGATGCTATATGTGAGCAACGAAAAATATTTGGAGCTGGCCAAATTGGAC 1287	1435 TGCGTTTACAAGCTACCTACGTGAACAATGAAAGTTTTACAGCTGGGAAAATAGAT 1494 1288 TTCAATATGGTGCAGGCCTTACACCAAAAGGAGCTCAAACAAA			1615 TAGCGGGGGGGGCCTATGAACCCCAGTATGCCAAGTTCCTCTTTACAAAGTG 1674 1468 TCTTGCCTGGCAGTTATTCTAGACGATCTTTAGGACACCCAGGATCTTTGGATGATCTT 1527	1675 GCATGCTAGCAGACTGTATGTATGACACTTATGGAACCCTAGATGGATTG 1734 1528 AAATTGTTCTGTGAAGCGGTCCGAAGATGGGATATCTCTCTGTGGTTAGGTCTGAAGTGGATATTGTTTTTTTT					1972 GAGTACATAAAGAATGGAATCACATCTATCGGCCAACGTATACTTCTGTTGAGTGGAGTG 2031 1828 TTTTTCACTGGAGAATTACTTCCTGATTACATTTACAGCAAGTAGACCTTGGGTCC 1884	2032 TTGATAATGGATGGGAACTCCTTTCGGAGGGGATTGAGAAAAGGTAGATAATTATCAGGA 2091 1885 AAATTTCTGCATCTTGTGTCTTTGACTGGAGGAGAAATCAATGACACCGAAGACT 1938	2092 AGACGTGTTCTCACAGAGTGAATAGCCTCATTTCCCGCCTGGGGGATGACACGAAGACA 2151 1939 TACCAGGCCGAGAGAAAACGTGGTGAATTGGTTTCCAGGGTACAGTGCTACATGAGGGAA 1998	2152 TATAAAGCTGAGAAGCTCGAGAAATTGGCGTCCAGCATTGAATGTTACATGAAAGC 2211 1999 AATCCGGAGTGGACAAGAGAAGAAGGTCTAAGTCATGTTATGGTATCATCGACAAGCG 2058	2212 CATCCTGAATGTACAGAGGAAGGGTCTCGATCACATCTATAGCATTCTGGAGCCGGCG 2271 2059 CTGAAGGAATTGAATTGGGAGTTGGCCAACCCCAGGGGGGGAGTGCCCATTGTGTGTG	2272 GTGAAGGAACTGACAAGAGTTTCTGAAGCCCGACGACGTCCCATTCGCCTGCAAG 2328
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	Sequence 2525 BP; 749 A; 498 C; 600 G; 678 T; 0 U; 0 Other; Query Match 32.3%; Score 723.4; DB 2; Length 2525; Best Local Similarity 59.8%; Pred. NO. 4.2e-214; Tudels 21; Gaps 6;	O; mismatches 8.1; indeid 27 C.E. ACAGCTTGGGGGGGGGAATTCGGTCATTGACGGCTCTGGT 50		151 TGGGGTGAGGATTGTTCTGGCGTATGACAGAGTTTTAAACACTCTCGCCTGCCT		GACTT	328 GAGGTCGTGTTTCCTGCAATGTTAGATGAAGAAAAGGTTGGGATTGGATCTTCCTTAT 387 11	388 CACCTCCCTTTCATCTCCCAAATCCACAAAAGCGCCAGAAAAAGCTTCAAAAGATTCCC 447	448 CTCAATGTTCTTGATAACCATGAGAGGTTTGCTCTACTCTCTGGAGGGTTTGCAAGAI 507	SOB GTGGTGGACTGGCAAGAGATCACAAATCTTCAATCAAGAGGGGACGGATCATTTTAAAGCTC 567718 ATAGTTGAATGGGAACGAATAATGGAAGTTCAAAGTCAGGATGGGTGTTCTTAAGCTCT 777		628 AACTICGIGCICAGCAAAITIGGCGACIACGIITCCITGCCAITGAICIAIT 687	688 GAACGCCTCTGGGCTGTCGALAACGCTTGGGAATCGATCGCTATTTCAAGAAA 747 	748 GAAATCAAAGAATCTGGATTACGTTTATAGGTACTGGGACGCCGAAAGAGGCGTGGGA,607 		868 AGACTICAIGGAIACAAIGIAICTICAGAIGIAITICAGAGAATITCAGAGAAAGGA 527	928 GACTICTITIGCTITIGCCGGTCAAACGCAAAITGGTGTGACCGATAATCTTAACCTITAT 987 	988 AGATGTTCACAAGTATGTTTTCCGGAGAAAAGATAATGGAAGAAGCTAAAGACCTTCACT 1047
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Query Match
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            2178
                        This is the nucleotide sequence of grand fir (Abies grandis) B-alphabisabolene-synthase CDNA. It codes for a wound-inducible enzyme (see AAY06566) that is capable of generating multiple sesquiterpenes. Capable of generating multiple sesquiterpenes. The full-length cDNA was obtained by 5'RACE from a wound-induced grand fir stem cDNA library. It differs from the sequence of clone AGI, provided in AAX87534, by a single nucleotide at position 194 (C is AGI, T in the present by a single nucleotide in an amino acid change from Ala-65 in AGI to Val-65 in the protein of AXY06566. The present sequence is believed to be the correct sequence of grand fir B-alpha-bisabolene synthase cDNA. The invention provides gymnosperm seguiterpene synthase mucleic acids and recombinant proteins, as well as expression vectors, and a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or modify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistence or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives
                                                       GGTATCTCTGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTTTTCGATCCTGTGGC 2237
                                                                      grand fir; sesquiterpene synthase;
disease resistance; fragrance; flavour; ss.
          AGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATGTACAGAGATGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grand fir (Abies grandis) sesquiterpene synthase genes and protein products, useful for sesquiterpenoid production.
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                                                                                                                                       AAX87529 standard; cDNA; 2528 BP
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gymnosperm; sesquiterpenoid;
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                                                       21;
                                                       Indels
Score 723.4; DB 2;
Pred. No. 4.2e-214;
0; Mismatches 871;
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Matches 1327; Conservative
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Abies grandis.
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This is the sequence of a computer-generated nucleic acid coding for a grand fir (Ables grandis) E-alpha-bisabolene synthase polypeptide (see AAY06568) that has conservative amino acid substitutions relative to the native E-alpha-bisabolene synthase sequence given in AAY06562. E-alpha-bisabolene synthase is a wound- inducible enzyme capable of generating multiple sesquiterpenes, especially E-alpha-bisabolene, from farnesyl diphosphate. The invention provides gymosperm sequiterpene synthase in a prokaryotic or eukaryotic host cell, and a method of imparting or enhancing production of a gymnosperm sequiterpene synthase in a prokaryotic or eukaryotic host cell, sesquiterpenoids, and hence to alter the flavour or fragrance of plant of products, to improve disease resistance or to alter ecological
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                                                                                                                                 2389 GCTGTTTCCAAATTAGAAGTCAAAGATCATATCAAAGAGTGTCTCATTGAACGCTGCC
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gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour;
                                                                       2179 GGIATCTCTGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTTTCGATCCTGTGGC
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231 GOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1375 AGAGTGGAAGCAAAGAGTACTGTCAAGTGTATCGCCCAGATTATGCACCATAGCAAAA 1434	1408 GTGGCGGTTAGTTTGGCGAGAATTCGCTGCTTGTAGAATTGCCAAGACT	1528 AAATTGTTCTCGAAGCGGTCCGAAGATGCGTACTCTGTGCTGGATAGCGTTCGGGAT 1587	1648 GGACTCAAGGAACAGGCCGTGATGTGCTGGGCTATCTTCGAAAAGTATGGGAGGGCTTG	1768 GAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCGACAGTCGTACTAAACTCCAATC 1827	TIGATAATGGATGGGCAACTCTTTCGCAAGAGCATTAGAGAAAGTAGATTATCCAGGA AAATTTCTGCATCTTGTCTTTGACTGGACCACTAATCAATGACATGAC	TACCAGGCCGAGAGAAACCGTGGATTGGTTTCCAGCGTACAGTGCTACATGAGGGAA	2212 CATCCTGAATGTACAGAAGGAAGGTCTCCGATCACATCTATAGCATTCTGGAGCCGGCG 2271 2059 CTGAAGGAATTGAATTGGAAGTTGGCCAÀCCCAGCGAGCAATGCCCCATTGTGTGTGTGAGA 2118 2272 GTGAAGGAACTGACAAGAGTTTCTGAAGCCGACGACGTCCCATTCGCTGCAAG 2328 2119 AGACTGCTGTTCAACACTGCAAGAGTGATGCTGTTTTATATGTACAGAGATGCTTT 2178	AAGATGCTTTTCGAGGGGGAGAGGGGGGGGGGGGGGGATGGAGGATGGAT	Т 8 1504
CGCCGGAATTICCCCAAACGTTGACTGATTTTGAAAAACGGTTAAAAGATGGTTCTTGTTCTTGTTTTTGTTCTTTGTTTTTTTT	8 8 8 8 8 8	8 8 8 8	8 8 8 8	8888	ጵ 8 8	8 6 8 8	6 8 6	8 6 8 6	8 & 8	RESUI AAX87
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1108 AAGGATCTTCCTGGAGGTGGAGTATGCTATAAAGTATCCGTGGCATAGAAGTATGCCA 1167
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1299 ACTABATATTTGAGAGAGGCTCTTGAGAAAGTGAGACTTCCAGTGCATGGAACAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 GCACCCCAATITCCCCAAACGCTTCAATGGATTCTGAACAATCAACTGCCAGATGGCTCG 150
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                                                                                                                                             Grand fir E-alpha-bisabolene synthase cDNA.
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                                                   2076 TIGATAATGGATGGGCAACTCCTTTCGCAAGAGGCATTAGAGAAGTAGATTATCCAGGA
                                                                                           GAATCGGGATTCAATGATCTTACATTCACCCGCCAGCGGCCTGTGGAAATGTATTTCTCA
                                                                                                                           1599 GATTCGGGGTTGCCACTATTCACCTTCGGTCGGAGAGGCCGCTGGAATTCTACTTCTTA
                                                                                                                                                            GTGGCGGTTAGTATGTTTGAGCCAGAATTCGCTGCTTGTAGAATTGCCTATGCCAAGACT
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AAT97447;

RESULT 9
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This sequence encodes a pacific yew taxadiene synthase (TS). The sequence can be used to increase taxol biosynthesis into taxoids in transformed cells. The mucleic acid sequences can be modified to produce proteins with improved efficiency, and to redirect the targeting of the expressed polypeptide. The modifications can be to alter catalytic efficiency, to modify substrate utilisation, and to alter product outcome. The antibodies specific for the mature native pacific yew TS polypeptide can be used to purify TS polypeptides, cloning TS homologues from Pacific yew or other plant species, and as probes for blots and immunoassays
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                                                                 Pacific yew; taxadiene synthase; taxol biosynthesis; probe; immunoassay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated terpene synthase (1)

comprising a region with at least 20% identity to region 265-535 of a 548

anino acid (as) sequence (1s), given in AAY99831. (1) contains nine alpha
carbon atoms (alphac) that have interatomic distances, between each
carbon atoms (alphac) that have interatomic distances, between each
other, within tabulated ranges, have a centre point (within a sphere of
radius 2.3 Angstrom) within tabulated ranges, and have an ordered
arrangement of R groups (defining as side chains), excluding specific
tabulated arrangements (tables given in the specification). (1), and
created enzymes, are used to produce a wide range of terpenoids (e.g.
cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances,
flavours, pheromones, defensive agents, pigments, antitumour agents,
flavours, pheromones, defensive agents, pigments, antitumour agents,
flavours pheromones and bile acids, as photoreceptors and as co-factor side chains.
Some synthases with little or no catalytic activity (and nucleic acids
corcoding then) are used as controls in the analysis of products formed by
enzymatic synthesis; as nutrient supplements; for affinity purification
of isoprenoids; or to develop immunological reagents or nucleic acids for
conjonents or synthases or inheritance of the gene in
plant breeding programs. The new synthases may produce novel terpene
products. AAA38910 to AAA38938 and AAY90831 to AAY9085 repersent
sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
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Pred. No. 1.7e-187;
0; Mismatches 903; Indels 42;
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Matches 1292; Conservative
immunological reagent;
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Pred. No. 5.6e-129;
0; Mismatches 631; Indels 30;
(-) -camphene synthas
(-) -pinene synthase;
nutrition; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-lalpha-pinene synthase, ilmonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding monoterpene synthases, for increasing synthesis in plants, e.g. for increasing resistance to pests or treatment of cancer.
                                                                                                                                                                                                                                                      Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; myrcene synthase; (-)-limonene synthase; terpinolene synthase; insect resistance; nutrition; ss.
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                                                                                                                                                                                            Grand fir monoterpene synthase coding sequence SEQ ID NO:
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Best Local Similarity 57.3%; Pred. No. 2.8e-118;
Matches 899; Conservative 0; Mismatches 620;
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BP.
AAF73421 standard; cDNA; 1890
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                                                                                                                                entry)
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P-PSDB; AAB69393.
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Fir monoterpene synthase clone AG3.48
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The sequences when expressed in transfected earsma properties, improvement of defense capability, and the alteration of chere ecological interactions mediated by mycrene, limonene, pinene, or their derivatives. In particular they can be used for the production of plant seeds for the extraction of oil or meal
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monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
probe; ss.
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                                                                                                                                                                     TGGCTTTGGTATCTCTGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTTTTCGATCC
TGTGAGAAGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATGTACAGAGA
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Synthase; protein co-ordinate data; active site; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isopremoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antitumour; steroid hormone; aignal transduction pathway; bile acid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent; ds.
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                                                            The present invention provides the protein and coding sequences of monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-limonene (-)-alpha-pinene synthase, ilmonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 GGCTGTCAAGAAGGATCTTCCTGGAGGTGGAGTATGCTATAAAGTATCCGTGGCATAG
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                                                                                                                                                                                                                                                                                                        Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 4.7e-117;
0; Mismatches 623;
                        English.
                           Example 3; Page 135-137; 175pp;
                                                                                                                                                                                                                                                                                                                                                                  Match 18.4%;
Local Similarity 56.8%;
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                                                                                                                                                                                                            .081 AACGCATTTGATAAGTGGGCTGTCAAGAAGGATCTTCCTGGAGAGGTGGAGTATGCTATA
                               CAAGTGAGAAGCATGTCGTTACTTCGAGCTTCAGAGATTTCGTTTCCCCGGAGAAAA
                                                                                          .021 ATAATGGAAGAAGCTAAGACCTTCACTACAAATCATCTCCCAAAATGCTCTTGCCAAAAAC
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                                                                                                                                        550 GTGATGGAAGAGGCCAAGGCATTCACAAGAAATATCTAAACCAAGTTTTAGCTGGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated terpene synthase (1)

Comprising a region with at least 20% identity to region 265-535 of a 348

Cambon atoms (alphac) that have interatomic distances, between each carbon atoms (alphac) that have interatomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angatrom) within tabulated ranges, and have an ordered arrangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (1), and crelated enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances, components of signal transduction pathways, precursors of steroid bormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids encoding them) are used as controls in the analysis of products formed by encoding them) are used as controls in the analysis of producic acids controling expression of terpene synthases may produce novel terpene products. AAA38918 cond AAY39031 to AAA38918 cond AAY39031 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to AAA3891 to 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        735
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Db 1540 GGCATCCTTAATCGTTCCTTGAGGAATTTAATTGGAAGTTTATGAAGGATAG---T 1596

Oy 2101 GCCCATTGTGTGAGAAGACTGCTTCAAGACTGAAGGTGATGCAGGTTTTAT 2160

Db 1597 GTCCCAATGTTGCAAGAATTCACTTTCAATATAGGTCGAGGTGTTTAT 2160

Oy 2161 ATGTACAGAGATGGTTTGGTATCTTCAAAAGAAGACCATGTCAGCCGAACT 2220

Oy 2221 CTTTTGATCAGAGACGCTTTATACATTTCTGACAAGAGAAGAAGACCAGATATTCAAAATT 1716

Db 1657 AAATACAGAGACGGCTTTATACATTTCTGACAAGGAAGAAGACCAGATATTCAAAATT 1716

Oy 2221 CTTTTGATCCAGT 2234

Db 1717 CTAGTCCACCAAGT 1730

Search completed: August 24, 2004, 21:15:27

Job time: 841.957 secs
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES	US-09-398-395A-55	US-09-887-586A-55	US-09-895-752-55	US-09-903-012B-55	US-09-900-797-55	US-09-234-393-1	US-09-360-545-15	US-09-865-171-1	US-09-398-395A-45	US-09-887-586A-45	US-09-895-752-45	US-09-903-012B-45	US-09-900-797-45	US-09-234-393-39	US-09-865-171-39	US-09-234-393-37	US-09-234-393-41	US-09-865-171-37	US-09-865-171-41	US-09-234-393-12	US-09-865-171-12	US-09-315-861-1	US-09-398-395A-43	US-09-887-586A-43	US-09-895-752-43	US-09-903-012B-43	US-09-593-253-1
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Sequence 55, Application US/09897586A Patent No. 6495354 GENERAL INPORMATION: APPLICANT: Chappell, Joseph APPLICANT: No. 64953541, Joseph P. APPLICANT: Starks, Courtney M.

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APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
RRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
STORMARE OF SEQ ID NOS: 58
SOFTWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 2861
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NAMB/KSY: CDS

LOCATION: (3)...(2606)

OTHER INFORMATION: abietadiene synthase
US-09-887-586A-55
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ORGANISM: Abies grandis
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378 AIGITTAGAIGTATGGGCTATGGCGAAACGAATCCCTCTGCATATGACACTGCTTGGGTA
                        GCAAGAATTCCGTCAATTGACGGCTCTGGGTGCACCCCAATTTCCCCAAACGCTTCAATGG
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                        CTIGCGACAGICGIACIAAACTCAATCTTTTCACTGGAGAATTACTTCCTGATTACATT 1860
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                                                                                                                       ATCAATGACACCAAGACTTACCAGGCCGAGAAAACCGTGGTGAATTGGTTTCCAGCGTA
                                                                         TTACAGCAAGTAGACCTTCGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTA
                                                                                       CAGTGCTACATGAGGGAAAATCCGGGAGTGCACAGGAAGAAGAAGCTCTAAGTTTAAT
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Best Local Similarity 68.8%; Pred. No. 0;
Matches 1544; Conservative 0; Mismatches 685; Indels 15;
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Sequence 55, Application US/09895752
Sequence 55, Application US/09895752
Sequence 55, Application US/09895752
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Coutrey M.
APPLICANT: Starks, Coutrey M.
APPLICANT: STARKS
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT APPLICATION NUMBER: US/09/995,752
CURRENT FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PRILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-01-23
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 55
LENGTH: 2861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase US-09-895-752-55
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ORGANISM: Abies grandis
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LOCATION: (3)
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Oy 2218 ACTCTTTCGATCCTGTGGCGTAG 2241	RESULT 4 US-09-903-012B-55 Sequence 55, Application US/09903012B Patent No. 6569656 GENERAL INFORMATION: APPLICANT: Chappell, Joseph APPLICANT: No. 65696561, Joseph APPLICANT: Starks. Courtney M.	; APPLICANT: Manna, Kathleen R.; TITLE OF INVENTION: SYNTHASES ; FILE REFERENCE: 07678-025001. ; CURRENT APPLICATION NUMBER: US/09/903,012B ; CURRENT FILING DATE: 2001-07-11 ; PRIOR APPLICATION NUMBER: 60/100,993 ; PRIOR FILING DATE: 1998-09-18	FRIOR APPLICATION NUMBER: 60/130,628 FRIOR FILING DATE: 1999-04-22 FRIOR FILING DATE: 1999-08-23 NUMBER OF SEQ ID NOS: 58 SOFTWARE: FastSEQ for Windows Version 3.0 LENGTH: 2861	; TYPE: DAA ; ORGANISM: Ables grandis ; FEATURE: ; NAME/KEY: CDS: ; OTHER INFORMATION: abietadiene synthase US-09-903-012B-55	Query Match 48.1%; Score 1078; DB 4; Length 2861; Best Local Similarity 68.8%; Pred. No. 0; Matches 1544; Conservative 0; Mismatches 685; Indels 15; Gaps 4; Qy ATGTTTCAGTCAGGGAGGGTGAAACGAATCCATCTGATAAACGATAGGTTGGGTG 0	61 GCAAGAATTCCGTCAATTGACGGCTCTGGTGCACCCCAATTTCCCCAAACGCTTCAATGG	Db 498 ATTCTTCAAAATCAGTTGAAAGATGGGTCAAGGGTGAAGGATTCTACTTCTTGGCTAT 557 Qy	618 ACACAAGTACAGAAAGGTATTGAATTCTTCAGGACACAAGCTGGAAAGATGGAAGATGAA 301 GCTGACAATCACAGGCCAAGTGGATTCGAGGTCGTGTTTCCTGCAATGTTAGATGAAGCA 678 GCTGATAGCCAAGTGGATTTGAAATAGTTTCCTGCAATGTTAGATGAAGCA	Oy 361 AAAACTTGGATTGCATCTCTTATCACCTTTCATCTCCCAAAG 420
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E: 1999-04-22 N NUMBER: 60/150,262 E: 1999-08-23 NOS: 58 Q for Windows Version 3.0 ell, Joseph 66457621, Joseph P. 66457621, Joseph P. 8. Courtney M. 18. Kathleen R. ON: SYNTHASES ON: SYNTHASES ON TOP 100, 197 110N NUMBER: US/09/900,797 110N NUMBER: US/09/398,395 111999-09-17 ation US/09900797

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ry Match 48.1%; Score 1078; DB 4; Length 2861; t. Local Similarity 68.8%; Pred. No. 0; c. c. s. s. s. s. s. s. s. s. s. s. s. s. s.	රු අ	1021 ATAATGGAAGAAGCTAAGACCTTCACTACAAATCATCTCCAAAATGCTCTTGCCAAAAAC 1080
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; Patent No. 6429014
; GREERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: PAPLIDES
FILE REFERENCE: wauri3885
CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT APPLICATION NUMBER: 60/052,249
EARLIER PILING DATE: 1999-07-26
EARLIER PILING DATE: 1999-07-16
EARLIER FILING DATE: 1998-07-10
EARLIER FILING DATE: 1998-07-10
EARLIER PILING DATE: 1998-07-10
SOFTWARE PAPLICATION NUMBER: PCT/US98/14528
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i LOCATION: (2)..(2350)
i OTHER INFORMATION: Clone AG1.28
US-09-360-545-15
                                                             Query Match 32.3%;
Best Local Similarity 59.8%;
Matches 1327; Conservative
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2168 GIGAAGGAACTGACAAGAGAGTTTCTGAAGCCCG---ACGACGTCCCATTCGCCTGCAAG
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Sequence 1, Application US/09865171

Patent No. 6451576

GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
CURRENT APPLICATION UNMBER: US/09/865,171
CURRENT APPLICATION NUMBER: US/09/244,393
PRIOR APPLICATION NUMBER: 60/072,204
PRIOR APPLICATION NUMBER: 60/072,204

PRIOR ELILING DATE: 1998-01-20

PRIOR ELILING DATE: 1998-01-22

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 59.8%; Pred. No. 3.8e-222;
Matches 1327; Conservative 0; Mismatches 871; Indels
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; TYPE: DNA
; ORGANISM: Abies grandis
US-09-865-171-1
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US-09-865-171-1
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1928 TIGATAATIGGAFGGGGAACTCCTTTCGCAAGAGGCATTAGAGAAAGTAGATTATCCAGGA 1987
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                                                                                                      1648 GGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAAAAGTATGGGAGGGCTTG 1707
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ORGANISM: Abies grandis
FEATURE:
NAME/KRY: CDS
LOCATION: (2)...(2347)
OTHER INFORMATION: R-alpha-bisabolene synthase
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Sequence 45, Application US/09398395A

Sequence 45, Application US/09398395A

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64687721, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT APPLICATION NUMBER: US/09/398,395A
CURRENT PELING DATE: 1999-09-17
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTESEQ FOR WINGOWS Version 3.0
SEQ ID NO 45
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                                                                                                                                                                                                  674 CCTGCTTCTACTGCCTGCGTTTTCATGCACACAGGAGACGCGAAATGCCTTGAATTCTTG 733
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                                    31 AATCCATCTGCATATGATACAGCTTGGGTGGCAAGAATTCCGTCAATTGACGGCTCTGGT
                                            Gaps
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           Length 2424;
                        Indels
          Score 723.4; DB 4;
Pred. No. 3.8e-222;
0; Mismatches 871;
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   AGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATGTACAGAGATGGCTTT
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; OTHER INFORMATION: B-alpha-bisabolene synthase US-09-887-586A-45
                                                                                                                                                                                        Sequence 45. Application US/09887586A
; Sequence 45. Application US/09887586A
; Patent No. 6495354
; GRMERAL INFORMATION:
   APPLICANT: Chappell, Joseph
; APPLICANT: Starks, Courtney M.
   APPLICANT: Starks, Courtney M.
   TITLE OF INVENTION: SYNTHASES
   FILE REFERENCE: 07678-02501
; CURRENT PILING DATE: 2001-06-22
   PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR APPLICATION NUMBER: 09/396,395
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR PILING DATE: 1999-04-22
; PRIOR PILING DATE: 1999-04-23
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                                                                                                                                                                                                                                                   Length 2424;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                   Score 723.4; DB 4;
Pred. No. 3.8e-222;
0; Mismatches 871;
LOCATION: (2)...(2347)
CTHER INFORMATION: B-alpha-bisabolene synthase US-09-895-752-45
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2119 AGACTGCTGTTCAACACTGCAAGAGTGATGCAGCTGTTTTATATGTACAGAGATGGCTTT 2178
                                                                                                                                                                                                                                                                                                                                                                   2225 AAGATGCTTTTCGAGGAGACAAGAGTGACGATGGTGATATTCAAGGATGGAGATGGATTC 2284
                                                                                                                                                           2168 GTGAAGGAACTGACAAGAGAGTTTCTGAAGCCCG---ACGACGTCCCATTCGCCTGCAAG 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2179 GGTATCTCTGACAAAGAGATGAAAGACCATGTCAGCCGAACTCTTTTCGATCCTGTGGC 2237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2285 GGTGTTTCCAAATTAGAAGTCAAAGATCATATCAAAGAGGTGTCTCATTGAACCGCTGCC 2343
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                                                       194 CGCCCGCAATTTCCCCAAACAGTTGACTGGATTTTGAAAAACCAGTTAAAAGATGGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (2) ... (2347)
; OTHER INFORMATION: B-alpha-bisabolene synthase US-09-903-012B-45
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GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 6566561, Joseph P.
APPLICANT: Starks, Coutney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT FILING DATE: 2001-07-11
PRIOR PELICATION NUMBER: 60/100,993
PRIOR PELICATION NUMBER: 60/130,628
PRIOR PELING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PELING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR PELING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/09903012B
Patent No. 6569656
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ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-903-012B-45
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Sequence 45, Application US/09900797

Sequence 4645762

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 6645761, Joseph
APPLICANT: Starks, Couttney M.
APPLICANT: Starks, Couttney M.
FILE REFERENCE: 07678-02501

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                                                                                                                             Query Match 32.3%; Score 723.4; DB 4; Best Local Similarity 59.8%; Pred. No. 3.8e-222; Matches 1327; Conservative 0; Mismatches 871;
                                                FEATURE:

NAME/KEY: CDS

LOCATION: (2)...(2347)

COTHER INFORMATION: B-alpha-bisabolene synthase
US-09-900-797-45
                        TYPE: DNA
ORGANISM: Abies grandis
SEQ ID NO 45
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Computer-generated nucleic acid sequence encoding
OTHER INFORMATION: E-alpha-bisabolene synthase
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Sequence 39, Application US/09234393A
Fatent No. 6265639
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Steek, John E
APPLICANT: Beter is Reinhard
APPLICANT: Steel, Christopher L
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF INVENTION: AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT FILING DATE: 1999-01-20
CURRENT FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE PATENT ON NUMBER: 60/072,204
SARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
LENGTH: 2525
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                                                                                                       TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Computer-generated nucleic acid sequence of THER INFORMATION: Computer-generated nucleic acid sequence of THER INFORMATION: E-alpha-bisabolene synthase
NAME/KEY: CDS
1. LOCATION: (1)..(2451)
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      PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 2525
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APPLICANT: Crock, John B
APPLICANT: Crock, John B
APPLICANT: Crock, John B
APPLICANT: Bohlmann, John B
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SEGUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
TITLE OF INVENTION: AND METHODS OF USE
FILE REPERENCE: WSIRL11468
CURRENT APPLICATION NUMBER: US/09/865,171
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/234,393
PRIOR APPLICATION NUMBER: 60/072,204
                                                                                                                                                      <u>AAATTGTTCTCTGAAGCGGTCCGAAGATGGGATATCTCTGTGCTGGATAGCGTTCGGGAT</u>
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acaartcatctccaaargctcttgccaaaacaacgcatttgaraagggctgtcaag 1107
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TTCAATATGGTGCAGGCCTTACACCAAAAGGAGACTCAACACTTGTCAGCTGGTGGAGA 1347
GAATGGGGATTCAATGATCTTACATTCACCGGCGGGCCTGTGGAAATGTATTTCTCA 1407
GIGGCGGTIAGIATGTITGAGCCAGAAITCGCTGCTTGTAGAAITGCCTATGCCAAGACT 1467
TCTTGCCTCGCAGTTATTCTAGACGATCTTTACGACACCCACGGATCTCTGGATGATCTT 1527
aaattgtictctgaaggggtcggaagatgggatatctgtggtggatagggttgggat 1587
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Publication No. US20020164736A1

GENERAL INPORMATION:

TELEL INPORMATION:

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE REPRENCE: PO2081US1

CURRENT FILING DATE: 2002-01-07

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 38

LENGTH: 2241
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APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase;
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase;
FILE REPERENCE: PO2081US1
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT PILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR PILING DATE: 2001-01-05
NUMBER: OF SEQ ID NOS: 41
SEQ ID NO 36
LENGTHARE: Patentin version 3.1
SEQ ID NO 36
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; SOFTWARE: Patentin version 3.; SEQ ID NO 32; LENGTH: 2622; TYPE: DNA; ORGANISM: Ginkgo biloba US-10-041-007-32
                                                                                                            Query Match 100.
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Matches 2241; Conservative
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Publication No. US20020164736A1

GENERAL INFORMATION:

APPLICANT: Matsuda. Selichi P.T.

APPLICANT: Schepmann, Hala G

TITLE OF INVENTION: Ginkgo Blloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1

CURRENT APPLICATION NUMBER: US/10/041,007

CURRENT PILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR PILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 41
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; Sequence 1, Application US/10041007
; Publication No. US20020164736A1
; APPLICANT: Mateuda, Selichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE NOF INVENTION: Ginkgo Biloba Levopimaradiene Synthase; FILE REFERENCE: PO2081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; ROOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 2705
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Patent No. US20020094556A1

GENERAL INFORMATION:
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APPLICANT: Manna, Kathleen R.
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1.COATION: (3)...(2606)
1. OTHER INFORMATION: abjetadiene synthase
US-09-887-586A-55
                                                                                         CTTTTCGATCCTGTGGCGTAG 2241
                                                                                                              CTTTTCGATCCTGTGGCGTAG 2644
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Matches 1544; Conservative
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US-09-903-012-05
US-09-903-012-05
Parent No. US20020094557A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 076-025001
CURRENT APPLICATION NUMBER: US/999,395
FRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
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                                                                                                                                                                                             15;
                                                                                                                                                             Length 2861;
                                                                                                                                                              Query Match
Best Local Similarity 68.8%; Pred. No. 0;
Matches 1544; Conservative 0; Mismatches 685; Indels
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 55
LENGTH: 2861
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
                                                                                     , NAME/KEY: CDS
LOCATION: (3)...(2606)
CTHER INFORMATION: abietadiene synthase
US-09-903-012-55
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2040 2160 2525 2411 2041 GGTATCATCGACACGCACTGAAGGAATTGAATTGGGAGTTGGCCAACCCAGCGAGCAAT 2100 2412 AGTGTCATGGAAATGCCCTCGAAGAGTTGAATAGGGAGTTTGTGAA-----TAACAAA 2465 1920 1980 1801 CTTGCGAÇAGTÇGTACTAAACTCAATCTTTTCACTGGAGAATTACTTCCTGATTACATT 1860 2231 cicrccaalairdarcgcgaartragaritctrcaacrcargggcriaacagggcgrig 2291 1680 2052 TACATTCAAAATGTTTGGAAAGTCCAACTTGAAGCTTACACGAAAGGAGAGAGGAGAATGGTCT 2111 GCAGCAAAGTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCATAGCA 1800 1620 1991 2051 2466 AIACCGGAIATTACAAAAGACTGGTTTTTGAACTGCAAGAATAATGCAACTCTTTAT 2101 GCCCCATTGTGTGTGAAAGACTGCTGTTCAACACTGCAAGAGTGATGCAGGTGTTTTAT CAGTGCTACATGAGGGAAAATCCGGAGTGCACAGAAGAAGAAGCTCTAAGTTTAT 1861 TTACAGCAAGTAGACCTTCGGICCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTA 1935 crarcacracreca --ccaaardccacacacaardaaararararrararek 1621 AACACAGTGAATGGATTTGGAAAAGATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGC 1992 AATACTTTTAATGATATAGCAAAGAAGGACGTGAGGCAAGGGCGCAATGTGCTAGGC TATCTTCGAAAAGTATGGGAGGGCTTGCTGCATCGTATACCAAAGAAGCCGAATGGTCG 1561 ATCTCTGTGCTAGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTAC 1441 GCTTGTAGAATTGCCTATGCCAAGACTTCTTGCCTCGCAGTTATTCTAGACGATGTTTAC GACACCCACCGATCTCTGATCTTAAATTGTTCTTGAAGCGGTCCGAAGATGGGAT 1695 CTICAAGAICTICGAAGGIGGIGGAAAICAICGGIITICACGGAICTGAAITICACICGI 1381 CAGCGCCTGTGGAATGTATTTCTCAGTGGCGGTTAGTATGTTTGAGCCAGAATTCGCT 2218 ACTCTTTCGATCCTGTGGCGTAG 2241 2112 2232 1981 1741 1815 1681 1501 셤 ઠે g ò 셤 ð g 8 ઠે 요 요 ð 셤 8 셤 Š 8 8 8 셤 Š g ઠે g ઠે g 8 a ò

Db 2586 TGCCTCTTCCAACCAGTTGCCTAG 2609

RESULT 10
US-10-041-018-365
Sequence 365, Application US/10041018
Sequence 365, Application US/204007233A1
SUBJICANT: MATSUGA, Selichi P.T.
APPLICANT: Matt, Elizabeth P.T.
APPLICANT: Hart, Elizabeth P.T.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547

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                                                                       ATCATGGAAGAAGCAAAACTCTGTACCGAAAGGTATCTGAGGAATGCTCTGGAAAATGTG 1454
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                                                   CTGGAGAATTTCAGAGACGAGAAAGGAGACTTCTTTTGCTTTGCCGGTCAAACGCAAATT
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larity 68.8%; Pred. No. 0;
Conservative 0; Mismatches 685;
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CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3.1
SEQ ID NO 365
LENGTH: 2861
                                                                                                                                    ; ORGANISM: Abies grandis
US-10-041-018-365
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Best Local Similarity
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Best Local Similarity 68.8%; Pred. No. 0;
Matches 1544; Conservative 0; Mismatches 685; Indels
                                                                                                                                                                                                                                                                                             Sequence 55, Application US/09893820
Fublication No US20040053386A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Rearks, Courtrey M.
APPLICANT: No. US20040053386A11, Joseph
APPLICANT: Starks, Courtrey M.
APPLICANT: Starks, Courtrey M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 0767-025001
CURRENT FILING DATE: 2001-06-28
CURRENT FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
SOFTWARE: FREESEQ for Windows Version 3.0
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NAME/KEY: CDS
LOCATION: (3)...(2606)
CTHER INFORMATION: abietadiene synthase
US-09-893-820-55
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ORGANISM: Abies grandis
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LENGTH: 2861
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Sequence 3, Application US/10041007; Publication No. US20020164736A1; GENERAL INFORMATION: APPLICANT: Matsuda, Selichi P.T.

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APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02001US1
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR PELING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
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Pred. No. 0;
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Best Local Similarity 68.8%;
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32.3%; Score 723.4; DB 9;
Best Local Similarity 59.8%; Pred. No. 6.8e-222;
Matches 1327; Conservative 0; Mismatches 871;
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US-09-887-586A-45
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                                                                                                    GGTGTGACCGATAATCTTAACCTTTATAGATGTTCACAAGTATGTTTTCCGGGAGAAAG 1020
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59.8%; Pred. No. 6.8e-222;
tive 0; Mismatches 871;
                                                                                                                                                               NAME/KEY: CDS

LOCATION: (2)...(2347)

TOTHER INFORMATION: E-alpha-bisabolene synthase

US-09-303-012-45
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: U8/09/903,012
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FESTESQ for Windows Version 3.0
SOFTWARE: 40454
                                                                                                                                                                                                          Query Match . 32.3'
Best Local Similarity 59.8'
Matches 1327; Conservative
                                                                                                                                                ORGANISM: Abies grandis
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                                 GAGGICGIGITICCIGCAAIGITAGAIGAAGCAAAAAGCTIGGGAITGGAICTICCITAI
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                                                                                              AAATTTCTGC-----ATCTTGTGTCTTTGACTGGACGACTAATCAATGACACCAAGACT 1938
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                               TITITICAC---TGGAGAATTACTTCCTGATTACATTTTACAGCAAGTAGACCTTCGGTCC 1884
                                                         TTGATAATGGATGGCGAACTCCTTTCGCAAGAGGCATTAGAGAAAGTAGATTATCCAGGA 1987
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OTHER INFORMATION: B-alpha-bisabolene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/09900797
Publication No. US20030087406A1
GENERAL INPOMMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: No. US20030084406A11, Joseph
APPLICANT: Rarks, Courtney M.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/900,797
CURRENT FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR PLING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER: OF SEQ ID NOS: 58
SEQUENCE: SEQ ID NOS: 58
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Matches 1327; Conservative
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ORGANISM: Abies grandis
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US-09-900-797-45
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NAME/KÉY:
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1631 AAGCTATTCACTGAGGCTGTGAGAAGATGGGACCTCTCCTTTACAGAAAACCTTCCAGAC 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1588 AATCAGTTGAAAGTTTGGTTCCTAGGGCTGTACACACAGTGAATGGATTTGGAAAAGAT 1647
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University of Florida, sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: JENREY (CAGGAAACAGCTATGACC).
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BX682869 Pinus pinaster differenciating xylem adult Pinus pinaster
CDNA clone 122H09 similar to Pinene synthase (EC 4.2.3.1), mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinus pinaster

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Coniferales; Pinasceae; Pinus,

Spermatophyta; Coniferopsida; Coniferales; Pinasceae; Pinus,

1 (Dases 1 to 730)

Canton, F.R., Le Provost, G., Garcia, V., Barre, A., Frigerio, J.-M.,

Paiva, J., Reveredio, P., Avila, C., Mouret, J.-F., Brach, J., de

Daruvar, A., Canovas, F.M. and Plomion, C.

Transcriptome analysis of wood formation in maritime pine

Unpublished (2003)
1331 TIGTCAGCTGGTGGAGAGAATCGGGATTCAATGATCTTACATTCACCCGCCAGCGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Э,
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ilarity 64.8%; Pred. No. 1.5e-78;
Conservative 0; Mismatches 254; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/mol_type="mRNA"
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/db_xref="taxon:71647"
/clone="122H09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pinus pinaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Frigerio JM
Genetique et Amelioration 69
                                                                                                             TTGGGAATCGATCGCTATT 739
                                                                                                                                                  BX682869.1 GI:38196667
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Bource

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/mol_type="mRNA"
/#mol_type="mRNA"
/#mol_type="mRNA"
/#mol_type="mRNA"
/#mol_type="mRNA"
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/#mol="cLaxon:3352"
/#mol="cLaxon:3352"
/#mol="mrnVa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 GTGGAGTATTCACTCAAATATCCCTGGCATAGAAGTATGCCAAGGCTGGAGGCCAGAAGC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AATGITITCAACGAAAAATATITGGAATTAGCAAAATITCAATCGACTGCAAGCI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 rinchchagachagacrichgannircaghagachagagantchicagachrichagag 362
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 TACGTTGAAAATTATGGACCAAAGGATTTCTGGATCGGAAAAATTTTGTATTTGATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1246 TATGTGAGCAACGAAAAATATTTGGAGCTGGCCAAATTGGACTTCAATATGGTGCAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 267.4; DB 14; Length
Pred. No. 9.3e-67;
0; Mismatches 181; Indels
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Zea mays CL2355_1 mRNA sequence.
AY109636 .
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Best Local Similarity 67.9%;
Matches 389; Conservative
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B. 1 (Bases I to 641)

B. 1 (Cordonnier-Pratt, M. -M., Lorenz, W. W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J., Ganon, R., Owen, A. and Neale, D.

EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)
Other ESTS: RTWW2 13 (12. bl A021
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAAACAGCTATGACC).
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CF475347.1 GI:34492719
                                                                                                                                                                                                                                                                                                                                                                                                                           ACGTGCCGTCCTATGATGATATATAGGGAACGCGAGTGTTTCAATAGCATTGGGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTACTAAACTCAATCTTTTCACTGGAGAATTACTTCCTGATTACATTTACAGGAAG
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                                                                                                                         ATGGATTTGGAAAAGATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCGAA
                                                                                                                                                                                      Arcabarcecreaagaacecegaaaacecagecercarcraciaecraecrracarracarracaa
                                                                                                                                                                                                                                                      AAGTATGGGAGGCTTGCTCGCATCGTATACCAAAGAAGCCGAATGGTCGGCAGCAAAGT
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TGGATAGCGTTCGGGATAATCAGTTGAAAGTTTGCTTCCTAGGGCTGTACAACACAGTGA
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Pinus taeda
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AATCTICAAICAAGAAGGAATCATTITIAAGCTCCCCTGCATCTACTGCTTGTGTCTTC
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Submitted (25-APR-2002) Maize Mapping Project, University of
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdD.inataeta.edu. TIGR,
www.igr.org; or NUSBI, www.ncbl.nlm.nlm.gov. When the source of the
maize CDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Takte, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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                                                              21; Gaps
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/db_xref="MaizeDB:630936"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone lib="Maize Mapping Project/DuPont Cornsensus Library"
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Pred. No. 6.3e-65;
0; Mismatches 786; Indels 21;
                                                      Panicoideae; Andropogoneae; Zea
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BF517045 MXSI (N8f Xylem Side wood Inclined) Pinus taeda CDNA clone NXSI 008 E08 F NXI (N8f Xylem Side wood Inclined) Pinus taeda CDNA clone NXSI 008 E08 5' similar to Arabidopsis thallana sequence At4902780 ent-Kaurene synthetase A - like protein see

1428

1592

1191

1071

1295

831

1118

651

1652

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629

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Unpublished (2003)
Other BSTS: RTDS3 2 A09. b2 A022
Contact: Cordonnier-Pratt FM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratterious.ed
Email: mmpratterious.ed
EMA: Prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
and have been trimmed to exclude polyA.
Seq primer: JENERRY (CAGGAAACACTATGACC).
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/clone="RTD53: 2 A09 A022"
/clone="RTD53: 2 A09 A022"
/lab_hot="NHIDB-TI-phage-resistant E. coli"
/clone lib="Drought-stressed loblolly pine roots D53"
/note="Vector: p5L1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from poly4+ RNA from drought-stressed loblolly pine (Pinus taeda) roots. Water was withheld from ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into p5L1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
                                                                                                                                                                                                                                                                                                                                                                                                 CF397293 175 bp mRNA linear EST 29-AUG-2003
RTDS3_2_A09.gl_A022 Drought-stressed loblolly pine roots DS3 Finus
taeda_cDNA clone RTDS3_2_A09_A022 5', mRNA sequence.
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                             301 ATCCANNNTGGGTCATTCCTCAGCTCGCCAGCATCTACAGCGGCTGTTTCATGCGTAC 360
                                                                                                                                                          361 AGGGAACAAAAATGCTNGNNNNTCTTGAATTTTGTCTTGAAGAATTCGGAAACCATGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopaida; Coniferales; Pinaceae; Pinus; Pinus.

    (bases 1 to 725)

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  540 ATCAAGAGACGGATCATTTTTAAGCTCCCCTGCATCTACTGCTTGTGTCTTCATGCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                         600 TCAAAACAAACGATGCCTCCACTTTCTCAACTTCGTGCTCAGCAAATTTGGCGACTACGT
                                                                                                                                                                                                              660 TCCTTGCCATTACCCACTTGATCTATTTGAACGCCTCTGGGCTGTCGATACAGTTG 715
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/mol_type="mRNA"
/strain="CCLONES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pinus taeda (loblolly pine)
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CF397293.1 GI:34355710
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AUTHORS
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CF397293
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                                                                                                                                                                                                                                                                                                                                     Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
C27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
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                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopaida, Coniferales, Pinaceae, Pinus, Pinus.

    (bases 1 to 476)

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    61 GGCTGATAGCCACAGGCCAAGTGGATTTGAAATAGTATTTCCTGCAATGCTAAAAGAAGC 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bmail: ron sederoff@ncsu.edu, jerri johnson@ncsu.edu
Please see http://web.ahc.umn.edu/blodata/nsfpine/ for further
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.
                                                                                                                                                                                                                                                      Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000)
Contact: Sederoff, Ron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db xref="taxon:3352"
/clone="NXSI_008_E08"
/tissue_type="Xylem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                    Pinus taeda (loblolly pine)
                                                BF517045.1 GI:11604507
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                                                                                                                               ORGANISM
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clone RS62E09, mRNA sequence.
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Prigatio, J. and Plomion, C. Indentification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach (Dupublishee (2002)
Contact: Frigatio JM
Genetique et Amelioration 69
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AATACGCCCTGAATACTTCTTGGCATGCCAGTGTCCCAAGAGTGGAAGCAAAAAGATACT
                                                                                                                                                          182 ACCAAGAAGAGATGAAGAGTGTTACCAGCTGGTTTAAAGATTCGGGGTTGCCTCTATTCA
                                                                                                                                                                                       1370 CATTCACCGGCCAGCCGGCTGGAAATGTATTTCTCAGTGGCGGTTAGTATGTTTGAGC
                            1190 TAGAGCAATTTGGATCAAATGATGTCTGGCTGGGGAAGACTGTGTATAAGATGCTATATG
                                                     grcaagtgtataatccggattatgcatgtttagcaaaaagtgtttacaagctgtcccacg
                                                                                                  route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
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CF397946 634 bp mRNA linear EST 29-AUG-2003 RTDS3 23 G06.gl A022 Drought-stressed loblolly pine roots DS3 Pinus taeda_cDNA clone RTDS3_23_G06_A022 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 ACATGAAAATATGTTTTAAGGGTTTTTACAATACTTTTAATGAAATCGCTGAAGAAGGGG
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                                                                                                                                                                                                                                                                                                                                              9.6%; Score 214.8; DB 13; Length 583; 63.6%; Pred. No. 2.6e-51; arive 0; Mismatches 202; Indels 5;
                                                                         seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus taeda (loblolly pine)
Pinus taeda
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CF397946.1 GI:34356363
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.6
Matches 361; Conservative
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/mol_type="mRNA"
/errain="CcLONES"
/db_xref="taxon:3152"
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RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
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                                                                                                                                                                                                                                                                                                          1688 GAAAAGTATGGGAGGGCTTGCTCGCATCGTATACCAAAGAAGCCGAATGGTCGGCAGCAA 1747
369 ATACGGAAAACCTTCCAGACTATA---TGAAGCTATTACAAAATCTATTATGACATAG 425
                                                                                                                                                                                                                     426 TTCACGAAGTGGCCTGGGAGGCAGAAGGAACAGGGACGTGAATTACTTAGCTTTTCA 485
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Pratt, L., Cordonnier-Fratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
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Other ESTS: RTDS1 17 C03.b1 A015
Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
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Matches 371; Conservative
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/clone="RTDS3 23 G06 A022"
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/clone lib="brought-stressed loblolly pine roots DS3"
/clone lib="brought-stressed loblolly pine roots DS3"
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from poly4+ RNA from drought-stressed loblolly pine (Pinus taeda) roots. Water was withheld from ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREY (CAGGAAACAGCTATGACC).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopeida; Coniferales; Pinaceae; Pinus; Pinus. (bases 1 to 634)
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                                                                                                                                                                                                                                                                                                                                                                        Other BST8: KTD83 23 G06.bl A022
Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Science Building, Rm. 2502, Athens, GA 30602-7271, USA
Pel: 706 542 1860
Pax: 706 583 0210
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Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J.
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/strain="CCLONES"
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Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
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RNA prepared.and library constructed by W. Walter Lorenz, School
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Other ESTS: RTWW2 7 B11.b1 A021
Contact: Corfoonier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Fax: 706 583 0210
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Porestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: JENBEY (CAGGAAACAGCTATGACC).
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Contact: Cordonnier-Pratt MM
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1929 CACCAAGACTTACCAGGCCGAGAGAAACCGTGGTGAATTGGTTTCCAGCGTACAGTGCTA 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1989 CATGAGGGAAAATCCGGAGTGCACAGAGGAAGAAGCTCTAAGTCATGTTTATGGTATCAT 2048
                                                                                                                  AAAAGTATGGGAGGCTTGCTCGCATCGTATACCAAAGAAGCCGAATGGTCGGCAGCAAA 1748
                                                                                                                                                                                                                                                                                                                                              1809 AGTCGTACTAAACTCAATCTTTTCACTGGAGAATTACTTCCTGATTACATTTTTACAGCA 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1869 AGTAGACCTTCGGTCCAAATTTCTGCATCTTGTGTCTTTGACTGGACGACTAATCAATGA 1928
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                                                                                                                                                                                                                                                                                                                                                                                                358 Arcaccarraccarracrascarcaccarcaccarraccraricarcarcarcarades 417
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                                                          178 AAATGAAATGTCTCAGGAGGCAGACAAGGCTCAAGGCCGAGACACGCTCAACTATTGTCG 237
                                                                                                                                                                                                                                                                                      298 TGAGGTGCCAACATTTGAGGAGTACTACGAGAACGGGAAAATTAGCTCTGGTCATCGCGT 357
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Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 TACGCGCTGCTACCAGGCGGACAGGGCCCCGTGGAAGAAGCTTCGTCTATATCTTGTTA
                                                                                                                                                                       238 ACAGGCTTGGGAGGAATATATTGATTCGTATATGCAAGAGGAAGCAAAGTGGATCGCCAGTGG
                                                                                                                                                                                                                                 1749 GTATGTGCCGACATTCAACGAATATGTGGAAAATGCCAAAGTGTCCATAGCACTTGCGAC
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     GAATGGATTTGGAAAAGATGGACTCAAGGAACAAGGCCGTGATGTGCTGGGCTATCTTCG
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Pinus taeda
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CF401916.1 GI:34360333
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Fax: 706 583 0210
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RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the

University of Florida; sequencing done in the Laboratory for

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-prime sequences are presented as their reverse complement

and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAAACAGCTATGACC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neale, D.
An EST database from well-watered loblolly pine (Pinus taeda) roots
                                                                                                                                                                                                    08-SEP-2003
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Pratt.L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and
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/lab_host="DHIOB-TI phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots WW3"
/note="Vector: pSil180; Site_1: EcoRI; Site_2: XhoI; The
library was prepared from polyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSil180. Inserts
excised with EcoRI (5' end) and XhoI (3' end).
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RTWW3_5 A06.gl_A022 Well-watered loblolly pine roots WW3 Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pred. No. 4.5e-44;
0; Mismatches 326; Indels
2044 ATCATCGACAACGCACTGAAGGAATTGAATTGGGAGTT
                                ATGGTCGATAACTTAACCAAGGAACTGAATTGGGAGTT
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Other ESTS: RTWW3 5 A06.bl A022
Contact: Cordonnier-Pratt MM
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Pinus taeda
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/strain="CCLONES"
                                                                                                                                                                                                                                                                                                              CF477103.1 GI:34505972
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Best Local Similarity 54.8%;
Matches 399; Conservative
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Fax: 706 583 0210
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                                                                                                                                                            /mol_type="mina"
/mol_type="mina"
/mol_type="mina"
/mol_type="mina"
/mol_type="mina"
/db xref="cGLONES"
/db xref="cGLONES"
/clone="RTWW1 15_805_A015"
/clone lib="WelloB-Typiage-resistant E. coli"
/clone lib="WelloB-Typiage-resistant E. coli"
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Pred. No. 1.3e-43;
0; Mismatches 302; Indel8 3;
           Seq primer: JENREV (CAGGAAACAGCTATGACC)
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                                                                                                                         /organism="Pinus taeda"
                                                              Location/Qualifiers
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Best Local Similarity 55.7
Matches 383; Conservative
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RESULT 13

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1690
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/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A mixture of genotypes were used.
Oligo-dT primed cDNA was directionally cloned into the
ECORI-ANDI lambda-ZAP vector arms and mass-excised to form
a pBluescript phagemid"
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31 bp mRNA linear EST 28-OCT-2003 cDNA clone RN41G08, mRNA sequence.
                                                                                                                                                                             Pinus pinaster
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta;
Coniferopsida; Coniferales; Pinaceae; Pinus;
I (bases I to 581)
Frigerio,J. and Plomion,C.
Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 186; DB 13; Length 5 ilarity 64.9%; Pred. No. 7.7e-43; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="mkNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      France
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/organism="Pinus pinaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
Seg primer: T3.
              581
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Frigerio JM
Genetique et Amelioration 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                       BX677599 RN Pinus pinaster
                                                                                                GI:38011551
                                                                                                                                                      Pinus pinaster
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SET.

Saccharum officinarum

Saccharum officinarum

Saccharum officinarum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum.

CE 1 (bases 1 to 688)

RS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

RS Vettore,A.L., da Silva,P.R., To (2001)

Contact: Arruda P

Contact: Arruda P

Contact: Arruda P

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Contact: Arruda P

Contact: Arruda P

Contact: Arruda Contact: Canpinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1137

Fax: 55 19 3788 1137

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Fax: 55 19 3788 1137

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Fax: 55 19 3788 1137

Fax: 56 19 3788 1137

Fax: 57 19 3788 1137

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Fax: 58 19 3788 1137

Seq primer: Colection Center (BCCC) at http://www.bcccenter.fcav.unesp.br

Plate: Col row: F column: 02

Seq primer: T' Promotor Primer.

Location/Qualifiers

RES

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1216 TGGCTGGGGAAGACTGTGTATAAGATGCTATATGTGAGCAACGAAAAATATTTGGAGCTG 1275
                                                                                                                                                                                                                                  979 AACCTTTATAGATGTTCACAAGTATGTTTTCCGGGAGAAAAGATAATGGAAGAAGCTAAG 1038
                                                                                                                                                                                                                                                                                                                                                                               1039 ACCTICACTACAATCATCICCAAAATGCTCTTGCCAAAAACAACGCATTTGATAAGTGG 1098
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                                                                                                                                                                                                                                                                                                   305 AACCTGAACAGGGCCTCTCAGGTAAGGTTCCCTGGAGGAGCACTTGTTGCAGGGTGCAGGG 364
                                                                                    919 GAGAAAGGAGACTTCTTTTGCTTTTGCCGGTCAAACGCAAATTGGTGTGACCGATAATCTT 978
                                                                                                                          245 AAGGACGGGGAGTTCTTCTGTTTCGTGGGGCAATCAACAACAAGCAGTCATCTGGGATGTAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 ATCATTGCTAAGGATCTACCAGGCGAGGTAAAATATACACTGGACTTCCCATGGTATGCA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 CGGCTGCTGCGGCTTCATGGATACGATGTCTCCCCAAGTGTATTTGGGAAGTT----TGAG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AGATTCTÓGTATGAGTTCCTTAGAGAAAGGGAAGCCCATGGCACGATTCGAGACAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1159 AGTATGCCAAGATTGGAGGCAAGAAGTTACATAGAGCAATTT---GGATCAAATGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 AGCTTACCGCGTGTAGAAGCAAGAGTCTACCTAGATCAATATGGCGGTGATAATGATGTC
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.

E 1 (bases 1 to 624)
S Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTS from developing seeds
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensetr. 3, 06466, Gatersleben, Germany
Tel: 039482-552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gub_species="valgare"
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HB20A66r BC Hordeum vulgare subsp. vulgare cDNA clone HB20A06
5-PRIME, mRNA sequence.
BU971902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TICAAGCAAGAAATCAAGCAGTGCTTGGATTATGTTCACAGGCACTGG---ACTGATGAG 127
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8.2%; Score 184.4; DB 13; Length 624;
Best Local Similarity 59.5%; Pred. No. 2.4e-42;
Matches 368; Conservative 0; Mismatches 241; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare subsp. vulgare"
|mol_type="mRNA"
|cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Error: 0.00
Plate: 20 row: A column: 6
552 ATGTGCCCTCCTTCAATGAATACATAGAGA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare subsp. vulgare
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                                                                                                                                                                                                                                                                                                                                                    58
plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 KD were directionally choned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                    9; Сарв
                                                                                                                                 Query Match

8.2%; Score 184.2; DB 14; Length 688;
Best Local Similarity 57.1%; Pred. No. 2.9e-42;
Matches 396; Conservative 0; Mismatches 288; Indels 9;
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Search completed: August 24, 2004, 15:24:15 Job time : 5673.28 secs

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August 17, 2004, 20:53:08; Search time 46.5386 Seconds (without alignments) 4529.153 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
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1 MFQSMGDGETNPSAYDTAWV......GISDKEMKDHVSRTLFDPVA 746 US-10-041-007-39 Perfect score:

BLOSUM62 Scoring table: Sequence:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ABU09779	AAY90858	ABB79393	ABU09780	AAW85703	AAY90853	AAB69373	ABB79392	AAY06567	AAY06566	AAY06562	ABB79391	ABU09781	AAY06568	AAW31655	AAY90852	ABB79394	ABU09782	AAY84104	AAB24916	AAR90848	ABB92819	AAR93800	AAY06569	AAY06571
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ALIGNMENTS

Levopimaradiene synthase; ginkgolide; enzyme; Escherichia coli; Candida albicans; Kluyeromyces lactis; Saccharomyces; maidenhair tree. Maidenhair tree levopimaradiene synthase. ABU09779 standard; protein; 873 AA. 07-JAN-2002; 2002US-00041007. 05-JAN-2001; 2001US-0259881P. Matsuda SPT, Schepmann HG; 06-AUG-2003 (first entry) (MATS/) MATSUDA S P T. (SCHE/) SCHEPMANN H G. WPI; 2003-352584/33. US2002164736-A1. Ginkgo biloba. 07-NOV-2002. ABU09779;

New purified and isolated nucleic acid sequence encoding a levopimaradiene synthase useful for producing pure ginkgolides in cells. Claim 20; Fig 4; 37pp; English. The invention relates to a purified and isolated nucleic acid sequence encoding a levopimaradiene synthase. The nucleic acid is used for the preparation of a ginkgolide in a cell, an expression vector, a unicellular organism (e.g. Saccharomyces, Escherichia coli, Candida albicans or Kluyeromyces lactis), a yeast host cell, a plant (particularly Ginkgo biloba), a host cell, a transgenic plant or a seed of the transgenic plant, for the biosynthesis of ginkgolides and in molecular biology, molecular genetics, and organic chemistry. The nucleic acid is capable of producing large amounts of pure ginkgolides in a cost-effective manner, particularly in an organism capable of a high-yield sjinkgolide-producing system. This sequence represents a levopimaradiene synthase polypeptide of the invention

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Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations.
signal transduction pathway; bile acid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent.
                                                                                                                                        KENT ) UNIV KENTUCKY RES DEPT.
(SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                               Chappell J, Manna KR,
                                                                                                                                                                              WPI; 2000-292839/25.
N-PSDB; AAA38937.
                                                      WO200017327-A2
                                       Abies grandis
                                                                                       17-SEP-1999;
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22-APR-1999;
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                                                                       30-MAR-2000.
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Pred. No. 0;
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108 746; Conservative
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Noel JP, Starks CM;

KENTUCKY RES DEPT 99US-0130628P. 99US-0150262P. 98US-0100993P. 99WO-US021419

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The present invention describes an isolated terpene synthase (I)

C comprising a region with at least 20% identity to region 265-535 of a 548

C comprising a region with at least 20% identity to region 265-535 of a 548

C carbon atoms (alphac) that have interatomic distances, between each carbon atoms (alphac) that have interatomic distances, between each cother, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom ) within tabulated arange, and have an ordered carangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and tabulated arrangements (tables given in the specification). (I), and constituted arrangements (tables given in the specification). (I), and constituted arrangements defensive agents, pigments, as fragrances, consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transduction pathways, precursors of steroid consponents of signal transducts and as co-factor side chains.

C components of signal transduction pathways, for muclesic formed by encoding them) are used as controls in memological reagents or nucleic acide for conjunction pathways, and as co-factor side for molicoring expression of terpene synthases or inheritance of the gene in products. AAA3810 to AAA3893 and AAV90831 to AAV90859 represent products.

C sequences used in the exemplification of the present invention
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Claim 112; Page 443-445; 450pp; English
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Synthase; protein co-ordinate data; active site; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isopremoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antitumour; steroid hormone;

Grand fir abietadiene synthase protein sequence SEQ ID NO:56.

(first entry)

25-AUG-2000 AAY90858;

AAY90858 standard; protein; 868 AA.

RESULT 2 AAY90858

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The present invention describes the heterologous expression of taxane analogues, comprising a DNA sequence comprising a taxane synthesis pathway, making a DNA construct in which the DNA sequence is under control of regulatory elements, introducing the DNA sequence is a host cell, growing the host cell to produce taxane analogues, and recovering the required taxane from the culture medium. Also described: (1) an isolated DNA sequence comprising the taxane synthesis pathway, the isolated DNA sequence; and (3) a host cell comprising the isolated DNA sequence; and (3) a host cell comprising a taxane synthesis pathway derived from a taxane-producing organism, plant or tree, the taxane synthesis pathway is foreign to the host cell. The taxane analogues have cytostatic activity, and so can be used as anticancer agents. The present sequence represents a taxadiene synthase homologues protein, which is given in an example from the present
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                      LENFRDEKGDFFCFAGQTQ1GVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKN 360
                                                                                                                                                        KYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFA 480
                                                                                                                                                                                                                                                                      Heterologous production of taxane analogs related compound useful as anticancer agent involves cloning a full-length taxane synthesis pathway from a taxan-producing organism into a taxane-resistant host cell.
                                                                                                                                                                      NTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIA
                                                                                                                                                                                                                                                                                                                                                                    NAPDKWAVKKOLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNE
          LGIDRYFKKBIKBSLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDV
                                                                                                                                                                                                                                                                                                        LATVVLNSIPFTGELLPDYILQQVDLRSKFLHLVSLTGRLINDTKTYQAERNRGELVSSV
                                                                                                                                                                                                                                                                                                                                                         QCYMRENPECTEEEALSHVYGI I DNALKELNWELANPASNAPLCVRRLLFNTARVMQLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taxane; taxane synthesis; taxadiene synthase; cytostatic; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taxadiene synthase homologous protein sequence q38710,
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2000US-0253843P.
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29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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The invention relates to a purified and isolated nucleic acid sequence encoding a levopimaradiene synthase. The nucleic acid is used for the preparation of a ginkgolide in a cell, an expression vector, a unicellular organism (e.g. Saccharomyces, Escherichia coli, Candida albicans or Kluyeromyces lactis), a yeast host cell, a plant (particularly dinkgo biloba), a host cell, a transgenic plant or a seec of the transgenic plant, for the biosynthesis of ginkgolides and in of the transgenic plant, for the biosynthesis of ginkgolides and in acid is capable of producing large amounts of pure ginkgolides in a costeffective manner, particularly in an organism capable of a highlyield ginkgolide-producing system. This sequence represents an abietaddene synthase polypeptide which shows similarity to the levopimaradiene synthase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSLGLDLPYHLPPISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLMAVDTVER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRVLNTLACLLTLXIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLDEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified and isolated nucleic acid sequence encoding a
levopimaradiene synthase useful for producing pure ginkgolides in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 MFRCMGYGETNPSAYDTAWVARIPAVDGSDNPHPPETVEWILGNQLKDGSMGEGFYFLAY
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                                                                                                                 Levopimaradiene synthase; ginkgolide; enzyme; Escherichia coli; Candida albicans; Kluyeromyces lactis; Saccharomyces; white fir; abietadiene synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.9%; Pred. No. 3.6e-235;
Matches 500; Conservative 107; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 4; 37pp; English
ABU09780 standard; protein; 868
                                                                                           White fir abietadiene synthase.
                                                                                                                                                                                                                                                                                  07-JAN-2002; 2002US-00041007
                                                                                                                                                                                                                                                                                                                  05-JAN-2001; 2001US-0259881P
                                                                                                                                                                                                                                                                                                                                                                                               Matsuda SPT, Schepmann HG;
                                                               entry)
                                                                                                                                                                                                                                                                                                                                                (MATS/) MATSUDA S P T. (SCHE/) SCHEPMANN H G.
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                                                               (first
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                                                                                                                                                                                                                         US2002164736-A1
                                                                                                                                                                                           Abies grandis.
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Length 868;

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Mycrene synthase; limonene synthase; pinene synthase; flavour;
monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
                                                                                                                                                                                                             NIVNGFCKDGLKEÇGRDVI.CYLRKVWEGLLASYTKEAEWSAAKXVPTFNEYVENAKVSIA 600
                                                                                                                                                                                                                       LENFRDEKGDFFCFAGQTQIGYTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKN 360
                                                                                                                                   421 KYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFA 480
                                                                                                                                               New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene.
SKDGSFLSSPASTAAVFMRTGNKKCLDFLNFVLKKFGNHVPCHYPLDLFERLWAVDTVER 365
                                                                                                                                                                                                                                                                                       LATVVINGIFFTGELL PDYILQQVDLRSKFLHLVSLTGRLINDTKTYQABRNRGELVSSV
                                                                                                                                                                                                                                                              361 NAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNE
                                                                                                        481 ACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNOLKVCFLGLY
                                                                                                                                                                                    LGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grand Fir monoterpene synthase clone AG1.28.
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N-PSDB; AAX08654.
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Nucleotide sequences encoding mycrene synthase, limonene synthase and pinene synthase from Grand fir may be incorporated into any organism (e.g. intact plant, animal, microbe), or derived cell-culture that produces geranyl diphosphate for the production of the aforementioned enzymes or their products. The sequences when expressed in transfected cells may also be used for the production or modification of flavour and aroma properties, improvement of defense capability, and the alteration of other ecological interactions mediated by mycrene, limonene, pinene, of other ecological interactions mediated by mycrene, limonene, pinene, of other ecological interactions of oil or meal. CDNAs encoding myrcene synthase, pinene synthase and limonene synthase from Grand Fir were isolated and sequenced by the following procedure. Based on comparison of sequences of different plant synthase enzymes, four conserved sequences were identified for construction of four degenerate primers (AAX08646 and AAX08648 and AAX08648) was an antisense primer and used for PCR with the other three sense primers only a combination of primers AAX08648 and AAX08649 generated a PCR product which was 110 base pairs in length. The amplified product was used in a plasmid construct to transform E.coll XII-Blue cells and the inserts were sequenced. Four probes (AAX08650-53) were devised from the sequenced insert and were used to screen a Grand Fir cDNA library. One of these clones is the myrcene appropriate in AAX08649. The other clones identified are Example 1; Page 90-92; 121pp; English. described in AAX08654-56

Sequence 782 AA;

53 37 38 GDGESMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIOSHFLLSDRL 6 GDGET--NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRV Gaps 6 Query Match 51.6%; Score 2050.5; DB 2; Length 782; Best Local Similarity 50.8%; Pred. No. 2e-175; Matches 379; Conservative 152; Mismatches 206; Indels 9; ઠે 셤

157 217 277 278 IYRHPEKBIKEALDYVYRHWN-ERGIGWGRLNPIADLETTALGFRLLRLHRYNVSPAIFD 336 64 LINTLACLLTLKIWIKGDIQVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS 122 LGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSR 182 DGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG 242 IDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLE 302 NPRDEKGDPFCPAGOTQIGVTDNLNLYRCSQVCPPGEKIMERAKTPTTNHLQNALAKNNA 362 98 LATLSCVLVLLKWINGDLQVEQGIEFIKSNLELVKDETDQDSLVTDFEIIFPSLLREAQS 218 DGSFLSSPASTACVFMHTGDAKCLEFLNSVMIKFGNFVPCLYPVDLLERLLIVDNIVRLG 243 123 183 303 ò g ò ద δ 셤 ઠ 셤 δ 셤

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719 695 629 Synthase; protein co-ordinate data; active site; modification; terpenoid; 603 TVVINSI-PFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS VQCYMRENPECTEBEALSHVYGI I DNALKBLNWELANPASNAPLCVRRLLFNTARVMQLF 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flavour; pheromone; defensive agent; pigment; antitumour; steroid hormone; signal transduction pathway; bile acid; affinity purification; photoreceptor; enzymatic synthesis; nutrient supplement; immunological reagent. Grand fir B-alpha-bisabolene synthase protein sequence SEQ ID NO:46. YMYRDGFGISDKEMKDHVSRTLFDPV 745 FENGEDGFGVSKLEVKOHIKECLIEPL 780 AAY90853 standard; protein; 782 AA 98US-0100993P. 99US-0130628P. 99US-0150262P. 99WO-US021419 25-AUG-2000 (first entry) WO200017327-A2 Abies grandis. 17-SEP-1999; 22-APR-1999; 23-AUG-1999; 18-SEP-1998 30-MAR-2000 720 755 AAY90853; 셤 ò g ò 셤

hydrocarbons, e.g. fragrances or antitumor agents, are derived from known enzymes by specific amino acid alterations. Novel terpene synthase enzymes, useful for producing terpene

Manna KR, Noel JP, Starks CM;

WPI; 2000-292839/25. N-PSDB; AAA38932

Chappell J,

INST BIOLOGICAL STUDIES

KENTUCKY RES DEPT

KENT) UNIV SALK

(SALK)

Claim 108; Page 418-420; 450pp; English.

The present invention describes an isolated terpene synthase (1)

comprising a region with at least 20% identity to region 265-535 of a 548

amino acid (aa) sequence (1a), given in AAY90811. (1) contains nine alpha
carbon atoms (alphaC) that have interatomic distances, between each
other, within tabulated ranges, have a centre point (within a sphere of
radius 2.3 Angstrom) within tabulated ranges, and have an ordered
arrangement of R groups (defining as side chains), excluding specific
tabulated arrangements (tables given in the specification). (1), and
cable arrangements (tables given in the specification). (1), and
capture, acylic, optionally hydroxylated), useful e.g. as fragrances,
clated enzymes, are used to produce a wide range of terpenoids (e.g.
cyclic, acylic, optionally hydroxylated), useful e.g. as fragrances,
components of signal transduction pathways, precursors of steroid
components of signal transduction pathways, precursors of steroid
components of signal transduction pathways, precursors as dide chains.
Some synthases with little or no catalytic activity (and nucleic acids
encoding them) are used as controls in the analysis of products formed by
enzymatic synthesis; as nutrient supplements; for affinity purification

fir abietadiene synthase protein fragment SEQ ID NO:

Grand

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542
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                                                                                                                                                                                                                                                                            IDRYPKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLE 302
                                                                                                                                                                                                                                                                                        NFRDEKGDFFCFAGGTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNA 362
                                                                                                                                                           122
                                                                                                                                                                             157
                                                                                                                                                                                                 182
                                                                                                                                                                                                            of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthase or inheritance of the gene in plant breeding programs. The new synthases may produce novel terpene products. AAA18910 to AAA38938 and AAY90831 to AAA38910 to AAA38938 and AAY90831 to AAY90859 represent sequences used in the exemplification of the present invention
                                                                                                                     63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVVLNSI-FFTGELLPDYILOQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS
                                                                                                                                                                                                                                                                                                                                                         FDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKY
                                                                                                                                                                                                                                                                                                                                                                                                LELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFAAC
                                                                                                                                                                                                                                                                                                                                                                                                           LNTLACLLTLKIWNKGDIQVQXGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS
                                                                                                                                                                     TGTDT-PYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSR
                                                                                                                                                                                                                                      DGSFLSSPASTACVPWHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG
                                                                                                                                                                                                                                                 GDGET -- NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRV
                                                                                                                                 Gaps
                                                                                                  9,
                                                                               782;
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                                                                               Length
                                                                              51.6%; Score 2050.5; DB 3; Length
larity 50.8%; Pred. No. 2e-175;
Conservative 152; Mismatches 206; Indels
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The present invention describes the heterologous expression of taxane analogues, comprising cloning a DNA sequence comprising a taxane spithesis pathway, making a DNA construct in which the DNA sequence is under control of regulatory elements, introducing the DNA construct into a host cell, growing the host cell to produce taxane analogues, and recovering the required taxane from the culture medium. Also described:

(1) an isolated DNA sequence comprising the taxane synthesis pathway, (preferably taxol synthesis pathway); (2) an expression vector comprising the isolated DNA sequence, and (3) a host cell comprising a taxane synthesis pathway derived from a taxane-producing organism, plant or tree, the taxane synthesis pathway is forcign to the host cell. The taxane analogues have cytostatic activity, and so can be used as anticancer agents. The present sequence represents a taxadiene synthase
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RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSBAVRRWDISVLDSVRDNQLKVCFLGLYNT
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                                                                                                                                                             LINTLACLLTLKI WNKGDI QVQKGVEFVRKHMBEMKDBAD-NHRPSGFBVVFPAMLDBAKS
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homologous protein, which is given in an example from the present
invention
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                                                                 51.6%; Score 2050.5; DB 5; Length 782;
                                                                                        Indels
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                                                                                      Conservative 152; Mismatches 206;
                                                                           Pred. No. 2e-175
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                                                                             50.8%;
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                                          Sequence 782
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Matches 379;
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                                                                 Query Match
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                                                                                                                                    543 VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA
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                                                363 PDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKY
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/note= "conserved element, Asp residues function in
coordination of a divalent cation"
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gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    720 YMYRDGFGISDKEMKDHVSRTLFDPV 745
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790 FKDGDGFGVSKLEVKDHIKECLIEPL 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-458569/38.
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDRYPKKEIKESLDYVYRYWDARRGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 LINTLACLLTLKIMNKGDIQVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGSFLSSPASTACVFWHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG
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                                                                                             Location/Qualifiers
566. .570
/note= "conserved element, Asp residues function in
coordination of a divalent cation"
               gymnosperm; вевquiterpenoid; disease resistance; fragrance; flavour.
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51.6%; Score 2050.5; DB 2;
Best Local Similarity 50.8%; Pred. No. 2.2e-175;
Matches 379; Conservative 152; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                    Bohlman J, Jetter R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Page 98-101; 136pp; English.
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                                                                         Abies grandis
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This sequence represents the B-alpha-bisabolene synthase of grand fir (Abies grandis), a wound-inducible enzyme capable of generating multiple sesquiterpenes, especially B-alpha-bisabolene, from farnesyl diphosphare. The sequence differs from the sequence of B-alpha bisavolene synthase AGI (see AAY05562) by a single residue, AGI having an Ala residue at position (see AAY05562) by a single residue, AGI having an Ala residue at position acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, especially in a plant, in order to impart, enhance or endify production of sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance of alter ecological interactions mediated by
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This sequence represents the E-alpha-bisabolene synthase of grand fir (Abies grandis), a wound-inducible enzyme capable of generating multiple sesquiterpenes, especially E-alpha-bisabolene, from farnesyl diphosphate. Another deduced sequence (see AAY05565) for the enzyme has val at position 65. The invention provides gymnosperm sesquiterpene synthase nucleic acids and recombinant proteins, as well as expression vectors, and a method of imparting or enhancing production of a gymnosperm sesquiterpene synthase in a prokaryotic or eukaryotic host cell, sesquiterpenoids, and hence to alter the flavour or fragrance of plant products, to improve disease resistance or to alter ecological interactions mediated by farnesyl diphosphate and its derivatives
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                                                                                                                   grand fir; sesquiterpene synthase; disease resistance; fragrance; flavour.
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                                                                                      Grand fir E-alpha-bisabolene synthase
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AAY06562 standard; protein; 817
                                                                                                                   B-alpha-bisabolene synthase;
gymnosperm; sesquiterpenoid;
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                            243 IDRYFKKEIKESLDYYYRYWDAERGYGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLE 302
                                     NFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNA 362
                                                                                                                     RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNOLKVCFLGLYNT
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Taxane; taxane synthesis; taxadiene synthase; cytostatic; anticancer;
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                                                                                                                    ABB79391 standard; protein; 817
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2000DK-00001730. 2000US-0253843P. 16-NOV-2001; 2001WO-DK000763 (NOVO) NOVOZYMES AS WO200240694-A2 17-NOV-2000; 29-NOV-2000; 23-MAY-2002. Vind J; Heterologous production of taxane analogs related compound useful as

WPI; 2002-471624/50

The present invention describes the heterologous expression of taxane analogues, comprising cloning a DNA sequence comprising a taxane analogues, comprising cloning a DNA sequence comprising a taxane correct comprising a DNA construct in which the DNA construct into under control of required texanes, introducing the DNA construct into a host cell, growing the host cell to produce taxane analogues, and crecovering the required texane from the culture medium. Also described: recovering the required comprising the taxane synthesis pathway; (1) an isolated DNA sequence; and (3) a host cell comprising a taxane. The isolated DNA sequence; and (3) a host cell comprising a taxane comprised from a taxane-producing organism, plant or synthesis pathway derived from a taxane-producing organism, plant or tree, the taxane synthesis pathway is foreign to the host cell. The taxane analogues have cytostatic activity, and so can be used as anticancer agents. The present sequence represents a taxadiene synthase the control, which is given in an example from the present 730 719 629 VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA 602 422 491 482 551 253 DGSFLSSPASTACVFMHTGDAKCLEFLNSVMIKFGNFVPCLYPVDLLERLLIVDNIVRLG 312 IDRYFKKEIKESLDYYYRYWDAERGVGWARCNPIPDVDDTAMGLRILRIHGYNVSSDVLE 302 362 431 252 ncer agent involves cloning a full-length taxane synthesis pathway taxan-producing organism into a taxane-resistant host cell. **VOCYMRENPECTEREALSHVYGIIDNALKELNWELANPASNAPLCVRRLLFNTARVMOLF** TVVLNSI-PFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS NFRDEKGDFFCFAGGTQIGYTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNA LELAKLDFNMVQALHQKETQHI VSWWRESGFNDLIFTRQRPVEMYFSVAVSMFEPFAAC 363 FDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKY LINTLACLLTLKI WINKGDI QVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS TGTDT BYHL PFISQIHQKRQKKLQKI PLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSR DGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG ٠. د. Length 817; Query Match
51.6%; Score 2050.5; DB 5; Length
Best Local Similarity 50.8%; Pred. No. 2.2e-175;
Matches 379; Conservative 152; Mismatches 206; Indels English. Example 3; Fig 1; 60pp; Sequence 817 AA; 483 552 543 603 423 303 372 193 243 133 123 183 73 64 from a a g g ઠ 셤 ò ò ઠ ઠે 셤 Š 셤 Š 셤 8 셤 δ 요 ઠ 원 Š 셤

셤 δ 셤

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                                                                                                                                                                                                                               NPRDEKGDFFCFAGOTOIGVTDNINLYRCSQVCFPGEKIMBEAKTFTTNHLQNALAKNNA 362
                                                                                                                                                                                                                                                     363 FDKWAVKKOLPGEVEYAIKYPWHRSMPRLEARSYIEOFGSNDVWLGKTVYKWLYVSNEKY 422
                                                                                                                                                                                                                                                                                                                                              432 SSAWNNKQNLSQEIKYALKTSWHASVPRVEAKRYCQVYRPDYARIAKCVYKLPYVNNBKF 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA 602
    LRLGLPYDLPYIHLLQTKRQERLAKLSREBIYAVPSPLLYSLEGIQDIVEWBRIMEVQSQ 252
                                                                         DGSFLSSPASTACVFMHTGDAKCLEFLNSVMIKFGNFVPCLYPVDLLERLLIVDNIVRLG
                                               DGSFLSSPASTACVEMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 TVVLNSI-FFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNT
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gymnosperm; sesquiterpenoid; disease resistance; fragrance; flavour.
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566. .570
hote= "conserved element, Asp residues function in
coordination of a divalent cation"
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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731 IECYMKDHPECTEBEALDHIYSILEPAVKELTREFLKP-DDVPFACKKMLFEETRVTMVI 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified and isolated nucleic acid sequence encoding a
levopimaradiene synthase useful for producing pure ginkgolides in cells.
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Candida albicans; Kluyeromyces lactis; Saccharomyces; white fir;
E-alpha-bisabolene synthase.
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                                          720 YMYRDGFGISDKEMKDHVSRTLFDPV 745
                                                                    White fir B-alpha-bisabolene synthase
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                                                                                                                                                                                                   ABU09781 standard; protein; 817
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                                                                                                                                                                                                                                                                                               (first entry)
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SCHEPMANN H G.
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59 AYDRVLATLACLLTIKIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLD 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 LCDRLLINTTNSVIALSVWRTGHSQVQQGAEFIAENLRLLNEE-DELSPD-FQIIFPALLQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is a cloned pacific yew taxadiene synthase (TS) protein. The sequence can be used to increase to increase taxol biosynthesis into taxoids in transformed cells. The protein can be modified to improved efficiency, and to redirect the targeting of the expressed polypeptide. The modifications can be to alter catalytic efficiency, to modify substrate utilisation, and to alter product outcome. The antibodies puscific for the mature native pacific, yew TS polypeptide can be used to purify TS polypeptides, cloning TS homologues from Pacific yew or other plant species, and as probes for blots and immunoassays
                                                                                       Pacific yew; taxadiene synthase; taxol biosynthesis; probe; immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQSMGDGBTNPSAYDTAWVARIPSI - - DGSGAPQFPQTLQWILANQLPDGSWGBECIFL
TVVLNSI-FFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS
                    660 VQCYMRENPECTEEFALSHVYGIIDNALKELNWELANPASNAPLCVRRLLFNTARVMQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONA encoding Pacific yew taxadiene synthase - used to increase taxol
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A7.9%; Score 1901; DB 2;
Best Local Similarity 47.5%; Pred. No. 7.2e-162;
Matches 358; Conservative 149; Mismatches 219;
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                                                                                                                                                  720 YMYRDGFGISDKEMKDHVSRTLFDPV 745
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                                                                                                                                                                                                                                                                             AAW31655 standard; protein; 862
                                                                                                                                                                                                                                                                                                                                                                                   Pacific yew taxadiene synthase.
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N-PSDB; AAT97447.
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LATLSCVLVLLKWANGDLQVEGGIEFIKTNLELVKDETDQDSLVTDFEIIFPSLLREAOS
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                                                                                                                             (Abies grandis) sesquiterpene synthase genes and protein useful for sesquiterpenoid production.
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llarity 50.8%; Pred. No. 2.7e-175;
Conservative 152; Mismatches 206; Indels 9;
                                         Steele CL
                                           Jetter R,
                                                                                                                                                                                      Example 11; Page 104-106; 136pp; English
                                             Bohlman J,
                                                 Crock JE,
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ses 379; Conserv
                                                                                   WPI; 1999-458569/38
                                                                                                      N-PSDB; AAX87531
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                                                                                                                                296 DWNKIMRPQSKDGSPLSSPASTACVLANTGDEKCFTFLNNLLDKFGGCVPCMYSIDLLER
                                                                                 DWQEITNLQSRDGSFLSSPASTACVFWHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFER
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Search completed: August 17, 2004, 21:00:13 Job time : 49.5386 secs HS PACE IS BLANK

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                                                                 US-08-326-286-4
US-08-21-465-1
US-08-405-254-5
US-09-865-171-44
US-09-865-171-44
US-09-234-393-48
US-09-234-393-46
US-09-234-393-46
US-09-234-393-46
US-09-865-171-20
US-09-865-171-46
US-09-865-171-46
US-09-865-171-46
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US-09-903-0128-48
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Sequence 56, Application US/09398395A

Sequence 56, Application US/09398395A

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64687721, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT APPLICATION NUMBER: US/09/398,395A

CURRENT PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-06-23

PRIOR FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 56
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US-09-398-395A-56
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

6: /cgn2_6/ptodata/2/laa/RCTUS_COMB.pep:*
                           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Best Local Similarity 67.6%; Pred. No. 2e-270;
Matches 505; Conservative 103; Mismatches 134; Indels 5;
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Sequence 56, Application US/09887586A

Patent No. 6495354

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
TILE OF INVENTION: SYNTHAESE
FILE REPERENCE: 07678-025001
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 58

SOFTWARE FREE FREESEQ FOR Windows Version 3.0
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; ORGANISM: Abies grandis
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APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REPERRNCE: 07678-025001
CURRENT FILING DATE: 2001-06-29
RIOR APPLICATION NUMBER: 09/398,395
RIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
RIOR PILING DATE: 1998-09-18
PRIOR PLILING DATE: 1998-09-18
PRIOR PLILING DATE: 1998-09-18
PRIOR PLILING DATE: 1999-04-22
PRIOR PLILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FRASESQ for Windows Version 3.0
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LIENGTH: 868
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Patent No. 6559297
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set Local Similarity 67.6%; Pred. No. 2e-270;
ttches 505; Conservative 103; Mismatches 134; Indels
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Patent No. 656966
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 65696561, Joseph
APPLICANT: No. 65696561, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Wanna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012B
CURRENT FILING DATE: 2001-07-11
FPRIOR FILING DATE: 1998-09-18
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PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 868
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US-08-900-797-56
Sequence 56, Application US/09900797
Patent No. 6645762
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                                                                                                         Sequence 16, Application US/09360545 Patent No. 6429014 GENERAL INFORMATION:
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; ORGANISM: Abies grandis
US-09-360-545-16
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LENGTH: 782
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                   APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TILLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395
FRIOR APPLICATION NUMBER: US/09/398,395
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR FILING DATE: 1999-04-22
FRIOR APPLICATION NUMBER: 60/150,262
FRIOR APPLICATION NUMBER: 60/150,262
FRIOR APPLICATION NUMBER: 60/150,262
FRIOR APPLICATION NUMBER: 60/150,262
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1999-08-23
FRIOR SEQ ID NOS: 58
FRIOR SEQ ID NOS: 58
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US-09-900-797-56
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LENGTH: 868
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483 RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNT 542 | : | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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APPLICANT: Croteau, Godney B
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: Steele, Christopher L
APPLICANT: Phillips, Michael A
TITLE ON INVENTION: MONOTRENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REPERENCE: wauri3885
CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER PILING DATE: 1999-07-10
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
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51.6%; Score 2050.5; DB 4; Length
Best Local Similarity 50.8%; Pred. No. 2.2e-200;
Matches 379; Conservative 152; Mismatches 206; Indels
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      397 SSAWNNKONLSQEIKYALKTSWHASVPRVEAKRYCQVYRPDYARIAKCVYKLPYVNNEKF 456
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                                               LELAKLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYPSVAVSMFEPEFAAC
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APPLICANT: Chappell, Joseph
APPLICANT: No. 64953541, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501.
CURRENT PEPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR PELLING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PSELSEQ for Windows Version 3.0
SSOFTWARE: PSELSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/09887586A Patent No. 6495354 GENERAL INFORMATION:
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ORGANISM: Abies grandis
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                                                              TVVLNSI-PFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS
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APPLICANT: Chappell, Joseph
APPLICANT: Sarks, Courtney M.
APPLICANT: Sarks, Courtney M.
APPLICANT: Sarks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REPERENCE: 07678-02501
CURRENT PELLING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FeatSEQ for Windows Version 3.0
SEMENTH: 782
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755 FKDGDGFGVSKLEVKDHIKECLIEPL 780
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Patent No. 6468772
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
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                                                                                363 FDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKWLYVSNEKY
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APPLICANT: (No. 65292911, Joseph
APPLICANT: No. 65292911, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 12091-06-29
PRIOR PILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-08-33
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FESTSEQ for Windows Version 3.0
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Patent No. 6559297
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US-09-895-752-46
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GDGBSMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIQSHFLLSDRL
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                                  INTLACLITIKIWNKGDIQVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS
                                                    US-09-903-012B-46

Sequence 46, Application US/09903012B

Sequence 46, Application US/09903012B

Sequence 46, Application US/09903012B

GENERAL INFORMATION:
APPLICANT: No. 65696561, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07679-02501
CURRENT APPLICATION NUMBER: US/09/903,012B
CURRENT FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 58

SEQ ID NO 46
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                                                                                                  38 GDGESMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIQSHFLLSDRL
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                                                  DB 4; Length 782;
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51.6%; Score 2050.5;
Best Local Similarity 50.8%; Pred. No. 2.2e
Matches 379; Conservative 152; Mismatches
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Patent No. 6445762
GENERAL INPORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 66457621, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
                  : ORGANISM: Ables grandis
US-09-903-012B-46
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US-09-900-797-46
LENGTH: 782
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CHARGNI FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: US/09/398,395

PRIOR FILING DATE: 1999-09-17

PRIOR PILING DATE: 1999-09-17

PRIOR PILING DATE: 1999-04-22

PRIOR FILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 46

LENGTH: 782
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US-09-900-797-46
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TYPE: PRT
CRGANISM: Abies grandis
US-09-234-393-38
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 GENERAL INFORMATION:
Factor No. 6265639
GENERAL INFORMATION:
FAPILICANT: Crockeau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Bohlman, Jorg
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APPLICANT: Bohlman, Jorg
FILLE REFERENCE: WSUR113345
CURRENT FILLING DATE: 1999-01-20
EARLIER FILLING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 55
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Best Local Similarity 50.8%; Pred. No. 2.4e-200;
Matches 379; Conservative 152; Mismatches 206; Indels 9;
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US-09-234-393-13
  US-09-234-393-13
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GENERAL INFOCRATION:
APPLICANT: Croceau, Rodney B
APPLICANT: Croceau, Rodne B
APPLICANT: Crock, John E
APPLICANT: Getter, Reinhard
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERRENE SYNTHASES FF
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR113145
CURRENT APPLICATION UNMER: US/09/234,393A
CURRENT APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-20
SEARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
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790 PKDGDGFGVSKLEVKDHIKECLIEPL 815
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APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
CURRENT APPLICATION NUMBER: US/09/865,171
CURRENT FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
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; TYPE: PRT
; ORGANISM: Abies grandis
US-09-865-171-13
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                                      660 VOCYMRENPECTEREALSHVYGIIDNALKELNWELANPASNAPLCVRRLLFRWTARVMQLF 719
                                                                                                                                                                                                                                                                                                            LGLDLPYHLPPISQIHQKRQKKTQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSR 182
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                                                                                                                                                                           603 TVVINSI-PPTGELLPDYILQOVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS
VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA
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CTHER INFORMATION: Computer-generated protein sequence US-09-234-393-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Croteau, Rodney B
APPLICANT: Croceau, Rodney B
APPLICANT: Crocex, John B
APPLICANT: Bohlman, Jorg
APPLICANT: Bohlman, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES F
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WGYN113345
CURRENT APPLICATION NUMBER: US/09/234,393A
CURRENT PILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER PILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PALENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/09234393A Patent No. 6265639 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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LENGTH: 817
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483 RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSBAVRRWDISVLDSVRDNQLKVCFLGLYNT 542 | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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Search completed: August 17, 2004, 21:03:50 Job time : 18.1272 secs

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121 KSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ 180
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                                                                                        August 17, 2004, 21:02:37; Search time 40.5485 Seconds (without alignments) 5775.546 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Sequence 14, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 386, Appl
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Sequence 182585,
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APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Schepmann, Hala G
TITLE OP INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: POZOBIUSI
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT APPLICATION NUMBER: US 60/259,881
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
SEQ ID NO 39
LENGTH: 746
TYBE: PRT
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2 US-09-893-820-46
3 US-10-041-007-16
3 US-10-042-007-16
3 US-10-042-16
4 US-10-042-144
US-09-903-1012-44
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches
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GENERAL INFORMATION:
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US-10-01-35
US-10-04-35
US-10-04-35
US-10-04-35
Sequence 35, Application US/10041007
Publication No. US20020164736A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Seiichi F.T.
APPLICANT: Schepmann, Hala G
TITLE COFINNENTION: Gillingo Biloba Levopimaradiene Synthase;
FILE REFERENCE: PO2031US1
CURRENT FILLING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR PILLING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 814
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100.0%; Score 3972;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches
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ORGANISM: Ginkgo biloba
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Sequence 37, Application US/10041007

SERERAL INFORMATION:
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Glinko Biloba Levopimaradiene Synthase
FILE REPERENCE: P02081US1
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881

PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41

SOPTWARE: Patentin version 3.1

FERSION NOS: 37
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Best Local Similarity 100.
Matches 746; Conservative
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; ORGANISM: Ginkgo biloba
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Sequence 2, Application US/10041007

Sequence 2, Application No. US20020164736A1

Publication No. US20020164736A1

SEQUENCE 2.

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase

TITLE OF INVENTION: DO2010107

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTION OF SEQ ID NOS: 41

SOFTWARE: PATENTION OF SEQ ID NOS: 41

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LENGTH: 873

TYPE: PRT
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; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Mateuda, Seiichi P.T.
; APPLICANT: Hart, Rilabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REPRENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Pacentin version 3.1
; SEQ ID NOS: 413
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                 100.0%; Score 3972;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                MYRDGFGISDKEMKDHVSRTLFDPVA 746
                       Best Local Similarity 100.
Matches 746; Conservative
; ORGANISM: Ginkgo biloba
US-10-041-007-2
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Sequence 33, Mpplication US/10041007
Sequence 33, Mpplication US/20020164736A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
FRICH FILING DATE: 2001-01-05

RESULT 6 US-10-041-007-33

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                                                                                           100.0%; Score 3972; 100.0%; Pred. No. 0;
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; Sequence 56, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, JOSeph
; APPLICANT: No. US20020094556A11, JOSeph
; APPLICANT: Starks, Courtney M.
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NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.3
LENGTH: 873
                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 746; Conservative
                                               TYPE: PRT
ORGANISM: Ginkgo biloba
                                                                       US-10-041-007-33
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126 MFRCMGYGETNDSAXDTAWVARIPAVDGSDNPHFPETVEWILQNQLKDGSWGEGFYFLAY 185
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                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094557All, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYMTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: 09/398,395
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FeatsEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 868
               842 MQGDGLTLSHDMEIKEHVKNCLFQPVA 868
                                                                                                              ; Sequence 56, Application US/09903012; Patent No. US20020094557A1; GENERAL INFORMATION:
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; ORGANISM: Abies grandis
US-09-903-012-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSLGLDLPYHLPPISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ
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APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 076-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
FRIOR APPLICATION NUMBER: 09/398,395
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR APPLICATION NUMBER: 60/130,628
FRIOR FILING DATE: 1999-04-22
FRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 56
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Gaps

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181 SRDGSFLSSPASTACVFWHTONKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER 240
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                                          LATVVLNSIPFTGELLPDYILQQVDLRSKFLHLVSLTGRLINDTKTYQAERNRGELVSSV
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                                                                                                QCYMRENPECTEERALSHVYGI I DNALKELNWELANPASNAPLCVRRLLFNTARVMQLFY
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il Similarity 67.6%; Pred. No. 8.7e-257;
505; Conservative 103; Mismatches 134; Indels
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GENERAL INFOGRATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, COURTNEY M.
APPLICANT: Starks, COURTNEY M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT APPLICATION NUMBER: US/09/993,820
CURRENT FILING DATE: 2001-06-28
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FELLING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
LENGTH: 868
                                                                                                                                                                                                                                                                                                                     721 MYRDGFGIS-DKEMKDHVSRTLFDPVA 746
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US-09-893-820-56
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Best Local Similarity 67.6%; Pred. No. 8.7e-257;
Matches 505; Conservative 103; Mismatches 134; Indels 5;
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US-09-900-797-56

Sequence 56, Application US/09900797

PUBLICALION NO. US20030087406A1

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Coutrney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07679-02501
CURRENT PELING DATE: 2001-07-06
FILING DAPLICATION NUMBER: US/09/980, 797
CURRENT PELING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-08-22
FRIOR FILING DATE: 1999-08-23

NUMBER: OF SEQ ID NOS: 58

SEQ ID NO 56

LENGTH: 868

TYPE: PRT
CORGANISM: Abies grandis
US-09-900-797-56
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                                                                SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER
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APPLICANT: Mateuda, Selichi P.T.
APPLICANT: Mateuda, Selichi P.T.
APPLICANT: Mateuda, Selichi P.T.
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
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Best Local Similarity 67.6%; Pred. No. 8.7e-257;
Matches 505; Conservative 103; Mismatches 134; Indels
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; TYPE: PRT
; ORGANISM: Abies grandis
US-10-041-007-4
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APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpne-Producing Unicellular Organism
FILE REFERENCE: PO2080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT PILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR PILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SEQ ID NO 388
LENGTH: 868
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Best Local Similarity 67.6%; Pred. No. 8.7e-257;
Matches 505; Conservative 103; Mismatches 134; Indels
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Publication No. US20040072323A1
GENERAL INFORMATION:
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US-10-041-018-388
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                                                                                                                                                                            LNTLACLLTLKI WNKGDI QVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS
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                                                                         GDGESMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIQSHFLLSDRL
                                                                                                      98 LATLSCVLVLLKWANGDLQVEQGIBFIKSNLELVKDETDQDSLVTDFEIIFPSLLREAQS
                                                        GDGET--NPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAYDRV
                       Query Match 51.6%; Score 2050.5; DB 9; Length Best Local Similarity 50.8%; Pred. No. 4.4e-190; Matches 379; Conservative 152; Mismatches 206; Indels
ORGANISM: Ables grandis
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                                   KSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ 180
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           SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER
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Fatent No. US20020094557A1
GENERAL INFORMATION:
APPLICANT: No. US20020094557A11, JOSEPH
APPLICANT: No. US20020094557A11, JOSEPH
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
TITLE OF INVENTION: GYNTHASES
TITLE REPERENCE: 07678-025501
CURRENT APPLICATION NUMBER: US/09/903,012
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APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: Starks, Courtney M.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07679-02501
FILE REFERENCE: 07679-02501
CURRENT PELLING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FELLING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
LENGTH: 782

Sequence 46, Application US/09897586A Patent No. US20020094556Al GENERAL INFORMATION:

US-09-887-586A-46

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CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-04-18
PRIOR PILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR PILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 46
LENGTH: 782
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ORGANISM: Abies grandis
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                                                                               HERERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: Chappell, Joseph
APPLICANT: No. US20030087406A11, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 0'678-02501
CURRENT PAPLICATION NUMBER: US/09/398,395
PRIOR APPLICATION NUMBER: 10/09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 58
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
                                         Sequence 46, Application US/09900797
Publication No. US20030087406A1
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; ORGANISM: Abies grandis
US-09-900-797-46
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Best Local Similarity
RESULT 15
US-09-900-797-46
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636 ILLLSGVLIMDGQLLSQBALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASS 695
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Search completed: August 17, 2004, 21:12:41 Job time : 42.5485 secs

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August 17, 2004, 20:57:35; Search time 14.7449 Seconds (without alignments) 4866.690 Million cell updates/sec Run on:

US-10-041-007-39 Title: Perfect score:

3972 1 MFQSMGDGBTNPSAYDTAWV.....GISDKEMKDHVSRTLFDPVA 746 Sequence:

BLOSUM62 Scoring table:

283366 seqs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ent-kaurene synthe	kaurene synthase A	ent-kaurene syntha	ent-kaurene syntina	hypothetical prote		hypothetical prote	vetispiradiene syn	limonene cyclase -	probable limonene	probable limonene	(+)-delta-cadinene	(+)-delta-cadinene	5-epi-aristolochen	sesquiterpene cycl	probable limonene	germacrene C synch	germacrene C synth	hypothetical prote	hypothetical prote	vetispiradiene syn	probable terpene s	hypothetical prote	hypothetical prote	_	_	_	hypothetical prote	probable vetispira
SUMMARIES	ID	D85035	T02959	T06783	T09672	G96825	T52059	A96637	A56118	A48863	F71434	G71434	868365	868366	T03714	T08174	H84633	T06266	T06265	E96723	H86460	C56118	G86443	T05328	C71424	G96588	T06285	C96642	T05329	T00509
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	Query Match Length	802	823	801	789	785	785	870		599		-								632	298	350	608	573	582	530	535	421	598	598
de	Query	33.2	32.6	32.1	26.9	25.8	25.8	17.7	16.7	16.6	16.5	16.4	16.3	16.2	15.9	15.9	15.9	14.2	14.1	11.8	11.6	11.3	11.2	10.5	10.2	•	8.6	•	9.4	4.6
	Score	1320	1293.5	1275.5	1066.5	1025.5	1025.5	704	663	099	654.5	650.5	647.5	643.5	m	633.5	633	565	559	469.5	460.5	448	443	416.5	403.5	393	89	388.5	375	374
	Result No.	1	7	е	4	ഗ	9	7	80	0	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	26	27	28	29

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DRVIATLACLLTLKIWNKGDIQVQKGVEFVRKHMBEMKDEADNHRPSGFEVVFPAMLDEA 120

104 ILRNLTDGEITISAYDTAWVALIDA--GDKTPAFPSAVKWIAENQLSDGSWGDAYLFSYH 161

1 MFQSMGDGBTNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGBECIFLAY

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SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER 240

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281 SQDGSFLFSPSSTAPAFMQTRDSNCLEYLRNAVKRFNGGVPNVFPVDLFEHIWIVDRLQR

121 KSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQBITNLQ 180

162 61

용 ઠે 셤 241 LGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDV 300

361 NAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQP-GSNDVWLGKTVYKMLYVSN

301 LENFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEBAKTFTTNHLQNALAKN 360

420 EKYLELAKLDFNINVQALHQXETQHIVSWWRESGFNDLTFTRQRPVEMYPSVAVSMFEPEF 479

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probable cyclase -	probable terpene s	vetispiradiene syn	hypothetical prote	hypothetical prote	hypothetical prote	ent-kaurene syntha	ent-kaurene syntha	y4kT protein - Rhi	hypothetical prote	probable terpene c	5-epi-aristolochen	hypothetical prote	protein C44B4.1a [conserved hypothet	hypothetical prote
H70972	F96684	B56118	T05331	T06287	D71424	JC7227	T00024	T10874	140214	H96525	T03982	T30951	D87757	C70034	S28279
~	~	7	N	~	~	~	N	~	~	~	~	N	~	~	~
501	598	300	612	471	383	952	946	516	216	203	148	1131	3864	757	1274
m.	6.3	8.8	8.8	8.3	7.9	6.8	6.2	5.5	4.9	4.2	3.8	3.4	3.4	3.1	3.1
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371 9	369	351.5	349.5	330.5	313	271	248	219.	193.	16	151.	Ï	13	122.	122.5

ALIGNMENTS

RESULT 1
popusa ent-kaurene synthetase A-like protein (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: D85035 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin-
Nature 402, 769-777, 1999
A; ILLE: Objective and mail/objective and mail/objective from A; Reference number: A85001; MUID: 20083488; PMID: 10617198
A;Accession: D85035
A;Status: preliminary
A!WOLECTLE FYPE: DNA A.Postidines : I-RD2 - STD3
A; Cross-references: GB:NC 001268; NID:q7269763; PIDN:CAB77763.1; GSPDB:GN00140
C,Genetics:
A;Gene: AT4g02780
A;Map position: 4
Query Match 33.2%; Score 1320; DB 2; Length 802;
Matches 281; Conservative 144; Mismatches 252; Indels 90; Gaps 17;

		RESULT 3 T06783 T06783 T06783 T06783 T06783 T06783 T06783 T06783 C;Species: Pisum sativum (garden pea) C;Species: Pisum sativum (garden pea) C;Species: Pisum sativum (garden pea) C;Dates: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Dates: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: T06783 R;Ait-Ali, T.; Swain, S.M.; Reid, J.B.; Sun, T.P.; Kamiya, Y. Plant, J. II, 443-454, 1997 A;Ritle: The LS locus of pea encodes the gibberellin biosynthesis enzyme ent-kaurene synt. A;Reference number: Z15810; MUD: 97260958; PMID: 9107034 A;Reference number: Z15810; MUD: 97260958; PMID: 9107034 A;Status: preliminary; A;Rocession: T06783 A;Status: preliminary A;Status: Dreliminary A;Status: L801 cAIT> A;Status: L801 cAIT> A;Experimental source: cultivar Torsdag C;Genetics: A;Gen	Query Match
	:::	Title: Cloning and characterization of the maize Anl gene. Reference number: 214794; MUID:95210929; PMID:7696880 Status: preliminary; translated from GB/EMBL/DDBJ Status: preliminary; translated from GB/EMBL/DDBJ Accession: T02959 Status: preliminary; translated from GB/EMBL/DDBJ Accession: T02959 Status: preliminary; translated from GB/EMBL/DDBJ Accession: T02959 Status: preliminary; translated from GB/EMBL/DDBJ Status: preliminary; translated from GB/EMBL/DDBJ Status: preliminary; translated from GB/EMBL/DDBJ Bone: ANI Punction: cyclase involved in gibberellic acid biosynthesis Duery Match 32.6‡; Score 1293.5; DB 2; Length 823; Bost Local Similarity 36.5‡; Pred. No. 1.5e-82; Astches 289; Conservative 146; Mismatches 243; Indels 113; Gaps Astches 289; Conservative 146; Mismatches 243; Indels 113; Gaps	219 278 237 338 397 · 357

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Gybecies: Arabidopsis thaliana (mouse-ear cress)

G'Species: Arabidopsis thaliana (mouse-ear cress)

G'Species: Arabidopsis thaliana (mouse-ear cress)

G'Species: Arabidopsis thaliana (mouse-ear cress)

G'Species: Arar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C'Species: Arar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C'ACCESSION: GS6825

R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hudhes, B.; Hufzar, L.

Anthors: Hunter, J.L.; Hudhes, B.; Hufzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzialli, R.; Alathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MulD:21016719; PMID:11130712

A;Recession: G96825

A;Returus: Preliminary

A;Molecule type: DNA

A;Residues: 1-785 <STO>

A;Residues: 1-785 <STO>

A;Residues: 1-785 <STO>

A;Consereferences: GB:AE005173; NID:g4835764; PIDN:AAD30231.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                        345 FSE---DIPPNCLGGYLKDFGA--SLELYKASQIITHPDESVLENINSWTSRFLKHGLSS 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::|||| ||| :| :| || :: :| 457 GHQDPLELAVEDFNTLQRIHLKELEELQRWYVENKLDELKFFRLHLGYCYFAAAATLTDP 516
                                                                                                                                                   | :||::|| ||| :| || || 232 SLFNSPSTTAAAFMHRNDDGCFDYLRSLLQKFDGSVPTIYPLDIYARLHMVDSLQKFGIA 291
                                                                                                                                                                                                                        RYFKKEIKESLDYVYRYM-DAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLEN 303
                                                                                                                                                                                                                                                          292 RHFKEEIRSVLDETYRCWMQGEE-----NIFLDASTCAMAFRMLRVEGYDVSSDQLTQ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 NNAFDKWAVKKD--LPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYV 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFL 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 ALHSTVCEIGRRALVWQGRSVMRNVIDGWLALLKVMRKEAEWSTNKVVPSMGEYMEQAHV 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIALATVVINSIFFIGELLPDYILOQVDLRSKFLHLVSLTGRLINDTKTYQAERNRGELV 657
                                        SFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGID
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Pred. No. 8.7e-64;
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Best Local Similarity
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QSQDGSFLPSPSSTAFALMQTKDGNCLKYLNNVVKKFNGGVPNVYPVDLPEHIWVVDRLE 335
                                                                                      300 VLENFRDEKGDFFCFAGOTQIGVTDNIALYRCSQVCFPGEKIMEEAKTFTTNHLQNALAK 359
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                                                      RIGIDRYFKKBIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | : | | | | : : : KE----LKGISC--QEN--ITNSEVESKMQELVQMVPQK-----
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RESULT 6
T152059
ent-Vaurene synthase (EC 2.5.1.-) [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52059
R;Yamaguchi, S.; Sun, T.; Kawaide, H.; Kamiya, Y.
Plant Physiol. 116, 1271-1278, 1998
A;Title: The GA2 locus of Arabidopsis thaliana encodes ent-kaurene synthase of SA;Reference number: Z25926; WUID:9820504; PMID:9536043
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                          ETNPSAYDTAWVARIPSIDGSGAPOFPQTLQWILNNQLPDGSWG---EECIFLAYDRVLN
                                                                                   TLACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLDEAKSLGL
                                                                                                                                            DLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGS
                                                                                                                                                                                                    FLSSPASTACVPMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDR
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                                                                                                                                                                                                                                                                                                                    NFRDEKGDFFCFAGQTQIGVTDN----LNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALA
 Gарв
47;
Mismatches 314; Indels
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 Conservative 146;
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MLYVSNEKYLELAKLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVS

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414 448

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---KNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEOFGS--NDVWLGKTVYK

MFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLK

474

VCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVE

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393 413 447 473 593 627 651 684

567

NRGELVSSVQCYMR-ENPECTEEEALSHVYGIIDNALKELN-WELANPASNAPLCVRRLL 709

685 AEGKL-NAVSLHMKHERDNRSKEVIIESMKGLAERKREBLHKLVLBEKGSVVPRECKEAF

NAKVSIALATVVINSIPPTGELLPDYILOQVDLR--SKFLHLVSLTGRLINDTKTYQAER

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288

YFKKEIKESLDYVYRYW---DAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDVLE 302

PLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLGIDR

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DLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSRDGS

289

303 NFRDEKGDFFCFAGQTQIGVTDN----LNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALA 340 PFAEESG----FSDTLEGYVKNTFSVLELFKAAQ-SYPHESALKKQCCWTKQYLEMELS

185 228

TLACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLDEAKSLGL

99

65

47;

Length 785;

ETNPSAYDTAWVARIPSIDGSGAPOFPOTLQWILNNOLPDGSWG---EECIFLAYDRVLN **ELSVSAYDTSWVAMVPSPSSQNAPLFPQCVKWLLDNQHEDGSWGLDNHDHQSLKKDVLSS**

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Query Match 25.8%; Score 1025.5; DB 2; Length Best Local Similarity 33.0%; Pred. No. 8.7e-64; Matches 250; Conservative 146; Mismatches 314; Indels

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hypotherical protein F11P17.15 [imported] - Arabidopsis thaliana (5gecies: Arabidopsis thaliana (mouse-ear cress) (5gecies: Arabidopsis thaliana (mouse-ear cress) (5gecies: Arabidopsis thaliana (mouse-ear cress) (5gecies: Arabidopsis thaliana (mouse-ear cress) (5gecies: Arabidopsis thalian-earson) (5,Accession: A96637 (Accession: A96637 (Accession: A96637 (Accession: A96637 (Accession: A); Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Creasy, T.H.; Dewar, K.; Anare 408, 816-820, 2000 (A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C., J. Li, J. H.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; A.; M.; Rowley, D.; Sakano, H. A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
FNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 746
                                                     LKMSKVLNLFYRKDDGF--TSNDLMSLVKSVIYEPVS
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-785 <YAM> A;Cross-references: EMBL:AF034774; PIDN:AAC39443.1 C;Genetics:

A;Gene: GA2 C;Keywords: transferase

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                                                                                                                                                                                                                                                                                                                                                                Gaps
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: A96637
A; A; Accession: A66637
A; Molecule type: DNA
A; Residues: 1-870 <STO>
                                                                                                                                                                                                                                                                                                   Query Match 17.7%; Score 704; DB 2; Length 870; Best Local Similarity 27.5%; Pred. No. 3.6e-41; Matches 219; Conservative 157; Mismatches 301; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                NPSAYDTAWVARIPS----IDGSGAPQFPQTLQWILNNQ-LPDGSW
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RESULT

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vetispiradiene synthase 1 - Hyoscyamus muticus (fragment)
C;Species: Hyoscyamus muticus
C;Species: Hyoscyamus muticus
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 29-Sep-1999
C;Accession: AS6118
Biol. Chem. 270, 7375-7381, 1995
A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus mut
A;Reference number: AS6118; MUID:95221394; PMID:7706281
A;Accession: AS6118
A;Accession: AS6118
A;Cession: AS6118
A;Cession: AS612
A;Molecule type: mRNA
A;Residues: 1-520 < CABC>
A;Cross-references: GB:U20188; NID:9763422; PIDN:AAA86337.1; PID:9763423
C;Superfamily: vetispiradiene synthase 1
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R;Colby, S.M.; Alonso, W.R.; Katahira, B.J.; McGarvey, D.J.; Croteau, R.
J. Biol. Chem. 266, 23016-23024, 1993
A;Tile: 48-limonene synthase from the oil glands of spearmint (Mentha spicata). CDNA is A;Reference number: A48863; MUID:94043077; PMID:8226816
A;Accession: A48863
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 NHLQNALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKT 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSLTGRLINDTKTYQA 649
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C;Species: Mentha spicata (spearmint)
C;Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 QEITNLQSRDGSFLSSPASTACVFWHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLW
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Length Indele

C; Superfamily: vetispiradiene synthase 1

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465 EMYESVAVSMPEPEFAACKIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVL 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 TINHLQNALAKNNAFDKWAVKKD---LPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDV 405
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                                                                                                                                                                                                                                                                                                                                      108 EELEMIDSLQRLGISYHYKHEIHDILRKIHDQHGEIER------ETQDLHATSLEFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 VPTFNEYVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSLTGRLINDT
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                                                                                                                                                                                                                                                       230 ERLWAVDTVERLGIDRYFKKEIKESLDYVY-RYWDAERGVGWARCNPIPDVDDTAMGLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 ANKRLSEFVAESS---KTICREDETYILEMVKRALETPYHWSIRRLEARWYI-----
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                                                  Query Match 16.5%; Score 654.5; DB 2; Best Local Similarity 31.1%; Pred. No. 6.1e-38; Matches 164; Conservative 105; Mismatches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Species: O3-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: F71434
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
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Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
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A;Accession: F71434
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                                                  A,Cross-references: GB:L13459; NID:g410229; PIDN:AAC37366.1; PID:g410230 C;Superfamily: vetispiradiene synthase 1
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                                                                                                                                                                                                                     Length 599
                                                                                                                                                                                                                Query Match 16.6%; Score 660; DB 2; Length 59 Best Local Similarity 31.0%; Pred. No. 2.5e-38; Matches 177; Conservative 101; Mismatches 219; Indels
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Best Local Similarity
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Drobable limonene cyclase - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
AyVariety: columbia
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BiBevan, M.; Barcroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk. P.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel. P.; Wedler, E.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A,Authors: Mueller-Auer, S.; Silvey, M.; Jamés, R.; Montfort, A.; Pons, A.; Funk Drobes, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans. C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A; Accession: G71434
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Recession: G71434
A;Stetus: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-1024 <BEV>
A;Crosetues: 1-1024 <BEV>
C;Genetics:
A;Map position: 4COP9-4G3845
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Matches 179;
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A, Map position: 4COP9-4G3845

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C;Species: Gossypium arboreum
C;Species: Gossypium arboreum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C;Accession: S68366
A;Chen, X.Y.; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch. Biochem. Biophys. 224, 255-266, 1995
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a can a 
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Pred. No. 3.2e-37;
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C;Species: Gossypium arboreum
C;Date: 19-Mar-1997 #text_change 29-Sep-1999
C;Dacession: S68365
R;Chen, X.Y.; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch. Biochem, Biochem, 255-266, 1995
A;Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a A;Reference number: S68365; MUID:96132653; PMID:8554317
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A;Experimental source: cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin blosynthesis
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                                                                                       A; Accession: S68365
A; Molecule type: mRNA
A; Residues: 1-554 < CHE>
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C;Superfamily: vetispiradiene synthase 1
                                                            644 TKTYQAERNRGELVSSVQCYMRENPECTEEALSHVYGIIDNALKELNWELANPASNAPL 703
                                                                                                                                                                                                                                                                                                                                                                                                                             NiAlternate names: sesquiterpene cyclase
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Sep-1999
C;Accession: T03714
R;Facchini, P.J.; Chappell, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11088-11092, 1992
A;Title: Gene family for an elicitor-induced sesquiterpene cyclase in tobacco. A;Reference number: 215024; MUID:93066390; PMID:1438319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445
193 YKPSFEEFKANALPTCGYAMLAITSFVGMGDIVTPETFKWAANDPKIIQASTIICRFMDD 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILRLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAKT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - SSIYDKEQSKANVLLRFAKLDFNLLQMLHKQELAQVSRWWKDLDFVTTLPYARDRVVEC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 VRDNQLKVCFLGLYNTVNGFGKDGLKEQGRD-VLGYLRKVWEGLLASYTKEAEWSAAKYV 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTFNEYVENAKVSIALATVVLNSIFFTGEL----LPDYILQQVDLRSKFLHLVSLTGRLI 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDTKTYQAERNRGELVSSVQCYMRENPECTEEEALSHVYGIIDNALKELNWELANPASNA 701
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|STIHLESAAPH-----LKSPLREQVTHALEQCLHKGVPRVETRFFI------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 LFERLWAVDTVERLGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTTNHLONALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKTVYKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGF-NDLTFTRQRPVEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-550 <FAC>
A;Residues: 1-550 <FAC>
A;Residues: 1-550 <FAC>
A;Cross-references: EMBL:L04680; NID:g170342; PIDN:AAA19216.1; PID:g505588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                   CVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 746
                                                                                                                                                                                                                             Query Match 15.9%; Score 633.5; DB 2; Best Local Similarity 29.0%; Pred. No. 1.6e-36; Matches 153; Conservative 118; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 37/3; 126/1; 251/2; 324/2; 370/3; 452/3
                                                                                                                                                                                                                                                                                                                                                                                                   5-epi-aristolochene synthase - common tobacco
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sesquiterpene cyclase (BC 2.5.1.-) - pepper
C;Species: Capsicum annuum (pepper)
C;Species: Capsicum annuum (pepper)
C;Species: Capsicum annuum (pepper)
C;Accession: 104174
R;Back, K.; Shin, D.H.; He, S.
Plant Cell Physiol. 39, 899-904, 1998
A;Title: Cloning and bacterial expression of sesquiterpene cyclase, a key branch point er A;Reference number: 216395; MUD:99033462; PMID:9816674
A;Reference number: 216395; MUD:99033462; PMID:9816674
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary
A;Nolecule type: mRNA
A;Status: 1559 <ABAC>
A;Cross-references: EMBL:AF061285; NID:93108342; PIDN:AAC61260.1; PID:93108343
C;Function:
A;Pathway: the synthesis of phytoalexin capsidiol
A;Note: unduced by uv vetispiradiene synthese 1
C;Superfamily: vetispiradiene synthese; transferase
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ALIGNMENTS

RESULT 1 TASY TAXER STANDARD; PRT; 862 AA. \rightarrow	28-FEB-2 28-FEB-2 28-FEB-2 28-FEB-2		Taxus brevifolia (Pacific yew). Eukaryota, Viridiplantae, Streptophyta, Embryophyta,	Spermatophyta, Coniferopsida, Coniferales, Taxaceae, NCBI_TaxID=46220;		"A cDNA clone for taxadiene synthase,	catalyzes the committed step of taxol biosynthesis. J. Biol. Chem. 271:9201-9204(1996).		MEDLIN		evolutionary implications.";	-!- FUNCTION: Catalyzes the cyclization of the ubiquitous isopre	C intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the C parent olefin with a taxane skeleton.	-1- CATALYTIC ACTIVITY: Geranylg	-	-!- SIMILARITY: Belongs to the terpene	This SWISS-PROT entry is copyright. It is produced throu	between the Swiss Institute of Bioinformatics and the EMBI	use by non-profit institutions as long as its content is in no most side of the content is in no most side of the content is the common of the content is the content of th	entities requires a license agreement (See http://www.is	or send		HSSP; Q40577; SEAU.	InterPro; IPR008930; Terp_cyc_torol InterPro; IPR001906; Terp_synth-lik	InterPro; InterPro;	Pfam; PF01397;	Taxol biosynthesis; Ly	ACT_SITE ACT_SITE	ACT_SITE 839 839 BY	
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Taxaceae, Taxus.
                                                    28;
                                  47.9%; Score 1901; DB 1; Length B ilarity 47.5%; Pred. No. 8.1e-125; Conservative 149; Mismatches 219; Indels
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28-FEB-2003 (Rel. 41, Last annotation update)
Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene
148 L -> V (IN REF. 2).
767 A -> V (IN REF. 2).
98303 MW, 9141B59780CD79A1 CRC64;
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Goerhardt B.;
Thesis (2001), Technische Universitaet Berlin, Germany.
-!- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid
-intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
parent olefin with a taxane skeleton.
-!- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene
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                                                                                                                                                           diphosphate.
--- PATHWAY: Taxol biosynthesis, first step.
--- SIMILARITY: Belongs to the terpene synthase family.
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InterPro; IRR008930; Terp cyc. toroid.
InterPro; IRR008106; Terp synth-like.
InterPro; IRR0080630; Terpene synth. C.
InterPro; IRR008949; Terpenoid synth. C.
Ffam; PP01397; Terpene synth, I.
Faxol biosynthésis; Lyase.
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"Cloning, expression, and characterization of taxadiene synthase, a
diteroene cyclase from Taxus chanses.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid
intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
parent olefin with a taxane skeleton.
--- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase)
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Taxus.
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    -1- PATHWAY: Taxol biosynthesis; first step.
    -1- SIMILARITY: Belongs to the terpene synthase family.

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B39 BY SIMILARITY.
98069 MW; 3A597BAF722BF679 CRC64;
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Spermatophyta, Coniferopsida, Coniferales, Taxaceae,
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InterPro; IPR001906; Terp_synth-like.
InterPro; IPR001905; Terpene synth C.
InterPro; IPR008949; Terpene synth Pfam; PP01397; Terpene synth; I.
Pfam; PP03936; Terpene synth; I.
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Matches 353; Conserv
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                                                                                                                               EAKSLGLDLPYHLPPISQIHQKRQKKL-----QKIPLNVLHNHQTALLYSLEGLQDVV 171
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MEDLINE=97413772; PubMed=9268308;
Bohlmann J., Steele C.L., Croteau R.;
"Monoterpene synthases from grand fir. (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
J. Biol. Chem. 272:21784-21792(1997).
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                                                                                                                                                                                                                         Abies grandis (Grand fir).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Abies.
VOL _TaxID=46611,
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GY---ESLNEMPYMMKKLLQLAKLEFNIFHSLQLRELQSISRWWKESGSSQLTFTRHRH 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVPTFNEYVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSLTGRLIND 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 WEDDFIQSLSSPYGGSSYSERAETVVEEVKEMFNSIPNNREL-----FGS---- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 DVWLGKTVYKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRORP 463
FUNCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene (C10) olefins blosynthesis.

CATALYTIC ACTIVITY: Geranyl diphosphate = limonene + diphosphate.

COFACTOR: Manganese and potassium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 PLDLFERLWAVDTVERLGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 YLPTFEEYLKNAKVSSGSRIATLQPILTLDVPLPDYILQEIDYPSRFNELASSILRLRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 GLRILRLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDN-LNLYRCSQVCFPGEKIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 VEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISV
                                                                                                                                                                                                                                                                                                                                                                                                                                        173 WQE--ITNLOS-RDGSFLSSPASTAC----VFMHTQNKRCLHFLNFVLSKFGDYVPCHY
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 637;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.1%; Score 1194.5; DB 1; Length Best Local Similarity 41.9%; Pred. No. 1e-75; Matches 244; Conservative 117; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                          CHLOROPLAST (POTENTIAL).
                                                                                            -!- SIMILARITY: Belongs to the terpene synthase family.
                                                                                                                                                                                                                                                                                                                                                                    8E80CD9DDE886898 CRC64;
                                                                                                                                                                                                                                                                                               Chloroplast
                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                        Interpro; IPR008930; Terp_cyc_toroid.
Interpro; IPR001906; Terp_synth-1ike.
Interpro; IPR005630; Terpene_synth_C.
Interpro; IPR008949; Terpenoid_synth.
Pfam; PF01397; Terpene_synth; I.
Lyase; Manganese; Transit peptide; Chlox TRANSIT
                                                          -1- PATHWAY: Oleoresinosis.
-1- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                             EMBL; AF006193; AAB70907.1; -.
                                                                                                                                                                                                                                                                                                                                                                     73477 MW;
                                                                                   -!- INDUCTION: By wounding.
                                                                                                                                                                                                                                                                                                                                                                    637 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 RILRLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMEEAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (C10) olefins blosynthesis.
--- CATALYTIC ACTIVITY: Geranyl diphosphate = myrcene + diphosphate.
--- COFACTOR: Manganese and potassium.
--- PATHWAY: Oleoresinosis.
--- SUBCELLULAR LOCATION: Chloroplast.
--- INDUCTION: By wounding.
--- SIMILARITY: Belongs to the terpene synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abies grandis (Grand fir).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Ables.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myrcene synthase, chloroplast precursor (EC 4.2.3.15)
                                               704 CVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U87908; AAB71084.1; -.
HISSP, Q40577; SEAS.
InterPro; IPR0018309; Terp_cyc_toroid.
InterPro; IPR001806; Terp_synth-like.
InterPro; IPR0050939; Terpene synth_C.
InterPro; IPR0050949; Terpene synth_C.
Pfam; PF01397; Terpene_synth; I.
Pfam; PF01396; Terpene_synth_C; IPR03968; Terpene_synth_C; IPR080899; Terpene_synth_C; IPR080899; Terpene_synth_C; IPR080899; Terpene_synth_C; IPR080899; Terpene_synth_C; IPR080899; Terpene_synth_C; IPR080899; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Terpene_synth_C; IPR080819; Te
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627 AA;
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024474;
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            241 IFSTRYLKBALOK-----IPVSALSQEIKFVMEYGWHTNLPRLEARNYIDTLEKDTSA 293
                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last amontation update)
Pinene synthase, chloroplast precursor (EC 4.2.3.14) (Beta-geraniolene synthase) ((-)-(18,58)-pinene synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=97413772; PubMed=9268308;
MEDLINE=97413772; PubMed=9268308;
Monoterpene synthases from grand fir (Ables grandis). CDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
J. Biol. Chem. 272:21784-21792 (1997).
---FINCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene (CIO) olefins biosynthesis. A mixture of alpha-and beta-pinene is
                                                  347 PYTLASCIAIDPKHSAPRLGPAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSSEIE
                                                                                                                                                                                               WLGKTVYKMLYVSNEKYLELAKLDFNWVQALHQKETQHIVSWWRESGFNDLTFTRQRPVE
                                                                                    MYPSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLD
                                                                                                                                 SVRDNOLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Abies.
NCBI_TaxID=46611;
706 RRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFD 743
                                                                                                                                                                                                                                                                                            :: |: |: |: |:||||| :::|| | || |: KKHAPDITRALHHLYIYRDGFSVANKETKKLVMETLLE 623
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InterPro; IPR008930; Terp_cyc_toroid.
InterPro; IPR001906; Terp_synth-like.
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HSSP; Q40577; 5EAT.
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Bukaryota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids;
Suromatophyta, Magnoliophyta, endicotyledons, core eudicots, rosids;
euromids II; Malvales, Malvaceae, Malvoideae, Gossypium.
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(+)-delta-cadinene synthase isozyme XC1 (EC 4.2.3.13) (D-cadinene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CV. Nanking;
SPRAIN=CV. Nanking;
CHEDLINE=9613263; PubMed=8554317;
CHEN X.-Y., Chen Y., Heinstein P., Davisson V.J.;
"Cloning, expression, and characterization of (+)-delta-cadinene
                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                              DB 1; Length 628;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                              23DBB788F3C8072C CRC64;
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                                                                                                                                   CHLOROPLAST (POTENTIAL) PINENE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1e-72;
97; Mismatches 179;
                                                                                                           Chloroplast
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                                                                                                                                                                                                                                                                                                                29.0%; Score 1151.5;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation updat
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InterPro; IPR005630; Terpene synth_C.
InterPro; IPR008949; Terpenoid_synth.
Pfam; PF01397; Terpene_synth_C; 1.
Byase; Manganese; Transit peptide; Chl
TRANSIT 1 ? CHLOROPLIA
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230, Conservative
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524
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531
554 AA;
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                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=29729;
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                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for scamercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibsib.ch).
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DVAEHKFKHRREDDCSAIECYMEEY-GVTAQEAYDVFNKHVESAWKDLNQEFLKP-TEMP 509
                                                                                                                                                                                                                                                                                                                                                                                                                               LRIHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDN----INLYRCSQVCFPGEKIMEE 344
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synthage: a catalyst for cotton phytoalexin biosynthesis.";
Arch. Blochem. Blophys. 324:255-266(1995).
-!- FUNCTION: Responsible for the cyclization of trans, trans-farnesyl diphosphate (FPP) to (+)-delta cadinene.
-!- CATALYTIC ACTIVITY: 2-trans, 6-trans-farnesyl diphosphate = (+)-delta-cadinene + diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERLWAVDTVERLGIDRYFKKEIKESLDYVY-RYWDAERGVGWARCNPIPDVDDTAMGLRI
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                        Length 554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEVLNRSLNLARVMDVLYREGDGYTYVGKAAKGGITSLLIEPIA 553
                                                                                                                                                                                                                                                                                                                                                                                              fatches 162; Conservative 103; Mismatches 210; Indels
                                                                           first (committed) step. SIMILARITY: Belongs to the terpene synthase family.
                                                                                                                                                                                                                                                                                                                                                  64137 MW; 59D6922DEDF9DCAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Score 647.5; DB 1;
Pred. No. 1.2e-37;
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                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                     HIATA SOCCESTY, SEAU.
INCEPPRO, IPRO08930; Terp_cyc_toroid.
InterPro; IPR001906; Terp_synth-like.
InterPro; IPR001906; Terpene synth.
InterPro; IPR008949; Terpenoid synth.
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                                                                                                                                                                                                                                                                                                                                                                        16.3%;
30.9%;
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MEDLINE-9612653; PubMed-8554317;

MEDLINE-9612653; PubMed-8554317;

MEDLINE-9612653; PubMed-8554317;

Cloning, expression, and characterization of (+)-delta-cadinene synthage: a catalyst for cotton phytoalexin biosynthesis.";

Arch. Biochem. Blophys. 324-255-266(1995).

I. FUNCTION: Responsible for the cyclization of trans, trans-farnesyl diphosphate (FPP) to (+)-delta cadinene.

CAPALYTIC ACTIVITY: 2-trans, 6-trans-farnesyl diphosphate = (+)-delta-cadinene + diphosphate.

I. PATHWAY: Phytoalexing gossypol and lacinilene C biosynthesis;
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                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase isozyme XC14 (EC 4.2.3.13) (D-cadinene
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STANDARD;
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Best Local
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                                                                                                                                                                                                                   453 VAEHKPKHRREDDCSAIECYMEEY-GVTAQEAYDVFNKHVESAWKDVNKEFLKP-TEMPT 310
                               VEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISV 523
                                                                           LDSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAK 383
                                                                                                     334 IDELPE-YMKPSYKALLDVYBEMEQLVAKHGRQYRVBYAKNAMIRLAQSYLVBARWTLQN 392
                                                                                                                                        YVPTFNEYVENAKVSIALATVVLNSIFFTGELLPDYILQQVDLRSKFLHLVSLTGRLIND 643
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Meng Y., Jia J., Liu C., Liang W., Zhou X., Heinstein P., Chen X.-Y.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl
diphosphate (FPP) to (+)-delta cadinene.
-!- CATALTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase isozyme C2 (RC 4.2.3.13) (D-cadinene
                                                                                                                                                                                                                                                              704 CVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 746
                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the terpene synthase family.
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15-JUL-1998 (Rel. 36, Last seq
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ACT_SITE 527 527
ACT_SITE 531 531
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Score 643.5;

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Query Match

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                                                                               LRLHGYNVSSDVLENFRDEKGDFPCFAGQTQIGVTDN----LNLYRCSQVCFPGEKIMEE
                                                                                                                                                                       121 LREHGYNVSCDVFNKFKDEQGNF-----KSSVTSDVQGLLELYQASYLRVHGEDILDE
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                   Gaps
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Starks C.M., Back K., Chappell J., Noel J.P.;
"Structural basis for cyclic terpene biosynthesis by tobacco 5-epi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÎS-JUL-1998 (Rel. 36, Created)
15-VUL-1998 (Rel. 36, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Ariscolchene synthase (EC 4.2.3.9) (5-epi-aristolochene synthase)
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family for an elicitor-induced sesquiterpene cyclase in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 89:11088-11092(1992).
No. 2.3e-37
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                 Matches 160; Conservative 105; Mismatches
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Pred.
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Science 277:1815-1820(1997).
30.3%;
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Similarity
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548 AA;
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                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-i- CATALYTIC ACTIVITY: Trans, trans-farnesyl diphosphate aristolochene + diphosphate.
-i- COFACTOR: Binds 3 magnesium ions per subunit.
-i- SUBUNIT: Monomer.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- INDUCTION: By fungal elicitor.
-i- SIMILARITY: Belongs to the terpene synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTON ACCEPTOR
                                                                                                                                                                                                                                                                                              EMBL; L04680; AAA19216.1; -.
PIR; T03714; T03714.
PDB; SEA7; 15-OCT-97.
PDB; SEA7; 12-NOV-97.
PDB; SEA7; 02-APR-98.
InterPro; IPR001930; Terp_cyc_toroid.
InterPro; IPR001930; Terp_cyc_toroid.
InterPro; IPR001930; Terpene synth.C.
InterPro; IPR008949; Terpene synth.C.
Pfam; PP01397; Terpene synth; I.
Pfam; PP013936; Terpene synth; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ^ ^ ^ ^ ^ ^ ^ ^
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274 VVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSYATYDELIPYTNAIERWDIK 333
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                                                                                                                                                                                       642 NDTKTYQAERNRGELVSSVQCYMRENPECTEEEALSHVYGIIDNALKELNWELANPAS-N 700
                                                                     PVEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDIS
                                                                                                                                                          523 VLDSVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDV-LGYLRKVWEGLLASYTKBAEWSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 TPVLCRSL--NLARVMDVLYREGDGYTHVGKAAKGGITSLLIDPI 553
PRT;
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                          220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LRFRLLREHGFDISCDAFNKFKDEAGN---FKASLTSDVQGLLELYEASYMRVHGEDILD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAKTFTTNHLONALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSN 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trans, trans-farnesyl
                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Nanking;
MEDLINE-97060798; PubMed=8904844;
Chen X.-Y., Wang W., Chen Y., Davisson V.J., Heinstein P.;
Choiling and heterologous expression of a second (+)-delta-cadinene synthase from Gossypium arboreum.";
J. Nat. Prod. 59:944-951(1996).
-I- FUNCTION: Responsible for the cyclization of trans, trans-farnesy diphosphate (FPP) to (+)-delta cadinene.
-I- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PATHWAY: Phytoalexing gossypol and lacinilene C biosynthesis;
                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase isozyme A (EC 4.2.3.13) (D-cadinene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
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// SIMILARITY.
7060C4F9D99412F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 631.5; DB 1 30.3%; Pred. No. 1.6e-36;
                                                                                           555 AA
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BY SIMILARITY
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InterPro; IPR001906; Terp_synth-like.
InterPro; IPR001906; Terpene synth C.
InterPro; IPR008949; Terpene synth, C.
Pfam; PP01397; Terpene synth; I.
Pfam; PP03936; Terpene synth, C; 1.
Lyase; Multigene family.
ACT_SITE 452 BY SIMILAR!
ACT_SITE 528 BY SIMILAR!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta-cadinene + diphosphate.
                                                                                                                                                                                                                                                                              Gossypium arboreum (Tree cotton)
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EMBL; U27535; AAB41259.1; -.
HSSP; Q40577; 5EAT.
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                                                                                           STANDARD;
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532 5
555 AA;
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                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29729;
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                                                                                      DCS3 GOSAR
Q43714;
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Matches 159
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                                             RESULT 11
DCS3 GOSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE, AND CHARACTERIZATION.
MEDLINE=96351891; PubMed=8728715;
Davis E.M., Tsuji J., Davis G.D., Pierce M.L., Essenberg M.;
"Purification of (+)-delta-cadinene synthase, a sesquiterpene cyclase from bacteria-inoculated cotton foliar tissue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phytochemistry 41:1044-1055(1996).

-I- FUNCTION: Responsible for the cyclization of trans, trans-farnesyl diphosphate (FPP) to (+)-delta cadinene.

-I- CATALYTIC ACTIVITY: 2-trans, 6-trans-farnesyl diphosphate = (+)-delta-cadinene + diphosphate.
                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Malvales, Malvaceae, Malvoldeae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis; first (committed) step.
-i- INDUCTION: By bacterial infection.
                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
(+)-delta-cadinene synthase (RC 4.2.3.13) (D-cadinene synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Westburn M;
Davis E.M., Chen Y.-S., Essenberg M., Pierce M.L.;
"cDNA sequence of a (+)-delta-cadinene synthase gene induced Gossypium hirsutum L. by bacterial infection.";
(In) Plant Gene Register PGR98-040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the terpene synthase family.
554 AA
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InterPro; IPR001906; Terp_synth-like
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601
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501 AA;
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                                                                                                                                                      RLHGYNVSSDVLENFRDEKGDFFCFAGQTQIGVTDN----LNLYRCSQVCFPGEKIMEEA 345
                                                                                                                                                                                                                         KTFTTNHLQNALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDV 405
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                                                                                                                                                                                                                                                                           EMYFSVAVSMFEPEPAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVL 524
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                                                                                                                                                                                                                                                                                                                                                                                                         393 YKPSFEEFKANALPTCGYAMLAITSFVGMGDIVTPETFKWAANDPKIIQASTIICRFMDD 452
                                                                                                                                                                                                                                                                                                                                                                                                                             644 TKTYQAERNRGELVSSVQCYMRENPECTEBEALSHVYGIIDNALKELNWELANPASNAPL 703
                                                                                                                                                                                                                                                                                                                                                                                                                                        453 VTEHKPKHRREDDCSAIECYMEEY-GVTAQEAYDVFNKHVESAWKDVNQGFLKP-TEMPT £10
                                                                                                                                                                                                      122 REHGFHVSCDVFNKFXDEQGNF-----KSSVTSDVRGLLELYQASYLRVHGEDILDEA 174
                                                                                                                                                                                                                                                                 WLGKTVYKMLYVSNEKYLELAKLDFNWVQALHOKETQHIVSWWRESGF-NDLTFTRQRPV
                                                                                                                                          RLWAVDTVERLGIDRYFKKEIKESLDYVY-RYWDAERGVGWARCNPIPDVDDTAMGLRIL
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of casbene synthase cDNA: evidence for conserved structural features among terpenoid cyclases in plants.";
Proc. Natl. Acad. Sci. U.S.A. 91:8497-8501(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Grreptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledona; core eudicots, rosida, eurosida I; Malpighiales, Euphorbiaceae; Acalyphoideae; Acalypheae;
                                                                                                                      49;
                                                                                                    554;
                                                                                                   DB 1; Length
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531 BY SIMILARITY.
64019 MW; BECC78ADBCA5BB16 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cabbene synthase, chloroplast precursor (EC 4.2.3.8).
Ricinus communis (Castor bean).
                                                                                                                      tches 158; Conservative 104; Mismatches 212;
                                                                                                           .7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AA
                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                  15.7%; Score 622.5; 30.2%; Pred. No. 6.7
InterPro; IPR005630; Terpene synth C. InterPro; IRR08949; TerpenoId synth. Pfan; PF01397; Terpene_synth, I. Pfam; PF03936; Terpene_synth, C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=9435958; PubMed=8078910; Mau C.J., West C.A.;
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                                                  451
                                                                              554 AA;
                                                                                                            Similarity
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                                        Lyase.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKIMEEAKTFTTNHLONALAKNNAFDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 QFGSNDVWLGKTVYKMLYVSNEKYLELAKLDFNMVQALHQKETQHIVSWWRESGF-NDLT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 FTRORPVEMYFSVAVSMFEPEFAACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVR 517
                    158 LYTAAIVFRVFRQHGFKMSSDVFSKFKDSDGK---FKESLRGDAKGMLSLFEASHLSVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 DLFERLWAVDTVERLGIDRYFKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDD----
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                                                                                                                                                                                                                                               diphosphate.
--- SUBCELLULAR LOCATION: Chloroplast.
--- INDUCTION: By oligogalacturonide fragments released by fungal infection. Detected after 5 h of incubation with the pectic fragments and reaches a maximum after 10-12 h.
--- RISCELLANBOUS: The Km of this enzyme is 1.9 micromol.
--- SIMILARITY: Belongs to the terpene synthase family.
--- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
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; F7B362D286747957 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
15.0%; Score 594.5; UB 1;
Best Local Similarity 27.6%; Pred. No. 6.7e-34;
Matches 149; Conservative 112; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASBENE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L32134; -; NOT ANNOTATED CDS.
InterPro; IPR008930; Terp_cyc_Foroid.
InterPro; IPR001906; Terp_synth-11ke.
InterPro; IPR005630; Terpene_synth_C.
InterPro; IPR008949; Terpene_synth.
Pfam; PP01397; Terpene_synth; I.
Pfam; PP03936; Terpene_synth, I.
MEDLINE=97115639; PubMed=8954576;
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231 SGIEGVVPNVWPINVFEPCWSLYTLHLAGL--FAHPALDEAVRVIVAQLDARLGVRGLGP 288
214 SKFGDYVPCHYPLDLFERLWAVDTVERLGIDRYFKKEIKESLDYVYRYWDAE---RGVGW 270
                                                                                                                                                                                                                                                                                                                                                                                                                                            328 ----VTFPGER----NASVSTNIHALHALRLLGKPAAGTSAYVEANRNPHGLWDNEK---- 376
                                                                                                                                                                               ARCNPI PDVDDTAMGLRILRLHGYNVSSDVLENFRDEKGDFFCFAGGTQIGVTDNLNLYR
                                                                                                                                                                                                                                                                                                                                                         331 CSQVCFPGEKIMEEAKTFTTNHLQNAL------AKNNAFDKWAVKKDLPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 VEYAIKYPWHRSMPRLEARSYIEQPGSNDVWLGKTVYKMLYVSNEK 421
                                                                                                                                                                                                                                  289 A-LHFAADADDTAVALCVLRLAGRDPAVDALRHF--EIGELF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein blr2149 (ORF7).
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Appl. Environ. Microbiol. 59:4136-4142(1993)
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Biochim. Biophys. Acta 1398:243-255(1998).
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YL49 BRAJA
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                                         TGRLINDTKTYQAERNRGELVSSVQCYMRENPECTEEEALSHVYGIIDNALKELNWELAN 596
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                                                                                                                                                                                                                        697 PASNAPLCVRR------LLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPVA 746
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24.2%; Pred. No. 7.8e-08;
tive 48; Mismatches 176; Indels 129; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 387:394-401(1997).
--- SIMILARITY: STRONG, TO B.JAPONICUM HYPOTHETICAL 55.4 kDa PROTBIN IN CYP117 3'REGION (ORP7).
--- SIMILARITY: Contains 2 PFTB repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiosis between Rhizobium and legumes.";
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Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
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Last annotation update)
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Hypothetical 64.4 kDa protein Y4KT
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Matches 113; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       STRAIN=USDA 110; PubMed=9655913; MEDLINE=98322110; PubMed=9655913; Tully R.E., van Berkum P., Lovins K.W., Keister D.L.; Identification and sequencing of a cytochrome P450 gene cluster from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
-!- SIMILARITY: Contains 2 PFTB repeats.
                                                                                                                                                                                                  STRAIN-USDA 110;
Tully R.B., Kaister D.L.;
"Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japonicum that is expressed anaerobically and
                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Interpro; IPR001330; Prenyltrans.
Interpro; IPR00830; Terp_cyc_toroid.
Pfam; PP00432; prenyltrans; 2.
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232 GIEGVPPNVWPINVFEPCWSLYTLHLAGL--PAHPALAEAVRVIVAQLDARLGVHGLGPA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 AYDRVLNTLACLLTLKIWNKGD-----IQVQKGVEFVRKHMEEMKDEADNHRPSGFEVV 112
                                                                                                                                                                                                                                                                                                                                                                              113 FPAMLDEAKSL--GLDLPYH---LPFISQIHQKRQKXLQKIPLNVLHNHQTALLYSLEGL 167
                                                                                                                                                                                                                                                                                                                                                                                                                 125 LPQFCGEAASLLGGVAFPRHPALLPL-----RQACLVKLGAVAMLPSGHPLLHSWEA- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 QDVVDW--QEITNLQSRDGSFLSSPASTACVFMHT-----QNKRCLHFLNF----VLS 214
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                                                                                                                                                                                                                                                         15 LLSEMSDGGSVGPSVYDTAQALRFHGNVTGR-----QDAYAWLIAQQQADGGWGSADFPL 69
                                                                                                                                         Query Match 5.1%; Score 204.5; DB 1; Length 516; Best Local Similarity 24.3%; Pred. No. 8.7e-07; Matches 113; Conservative 46; Mismatches 179; Indels 127; Gaps
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  1 protein; Repeat; Complete proteome.
45 86 PFTB 1.
401 443 PFTB 2.
134 134 S -> W (IN REF. 1 AND 2).
278 278 D -> B (IN REF. 1 AND 2).
516 AA; 55268 MW; D7A3A6D66860A761 CRC64;
Hypothetical p
REPEAT 40
CONFLICT 13
CONFLICT 27
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MEDILINE-21381393; PubMed=11488601;

Schepmann H.G., Pang J., Matsuda S.P.T.;

Cloning and characterization of Ginkgo biloba levopimaradiene synthase which catalyzes the first committed step in ginkgolide biosynthesis.";

Synthase which catalyzes the first committed step in ginkgolide biosynthesis.";

Arch. Biochem. Biophys. 392:263-269(2001).

RMBL; AF3131704; AALO9965.1;

RMBL; AP3131704; AALO9965.1;

RM GO; GO:0008152; P:Hyase activity; IEA.

GO; GO:0016829; F:Hyase activity; IEA.

RN GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR008949; Terpene synth.

RN InterPro; IPR001906; Terp_Cyc_foroid.

RN InterPro; IPR001906; Terp_Cyc_foroid.

RN Pfam; PP01397; Terpene—Synth.; 1.

RP Fam; PP03396; Terpene—Synth.; 1.

RN Pfam; PP03396; Terpene—Synth.; 1.

RN Pfam; PP03396; Terpene—Synth.; 1.

RN Pfam; PP03396; Terpene—Synth.; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Levopimaradiene synthase.
Ginkgo biloba (Ginkgo).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
NCBI_TaxID=3311;
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            InterPro; IPR08930; Terp cyc toroid.
InterPro; IPR081906; Terp synth-like.
Pfam; PP08432; prenyltrans; 1.
Pfam; PF01397; Terpene synth; 1.
Pfam; PP03936; Terpene synth C; 1.
SEQUENCE 868 AA; 99536 MW; AD5E79F56B70D25C CRC64;
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038710;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Abietadiene cyclase.
Abies grandis (Grand fir).
Abies grandis (Grand fir).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
NOTEL TAXID=46611;
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Stoffer-Vogel B., Wildung M.R., Vogel G., Croteau R.B.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 165768, AABOS407.1; -.
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GO; GO:0008125; P:metabolism; IBA.
InterPro; IPR00130; Prenyltrans.
InterPro; IPR005630; Terpene_synth_C.
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397 SSAWNIKQNI.SQEIKYALKTSWHASVPRVEAKRYCQVYRPDYARIAKCVYKLPYVNINEKF 456
QCYMRENPECTEBEALSHVYGIIDNALKELNWELANPASNAPLCVRRLLFNTARVMQLFY
                                              746
                                                           GO; GO:0016829; F.1yase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR005630; Terpenoid synth C.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008949; Terp_Gyc toroid.
InterPro; IPR001906; Terp_Gyc toroid.
InterPro; IPR001906; Terp_Gynth-like.
Pfam; PP01397; Terpene_synth; 1.
Pfam; PP03936; Terpene_Synth, 1.
                                             721 MYRDGFGIS-DKEMKDHVSRTLFDPVA
                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER
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                                                                                                                                                                                                                                                                                                                                               1 MPQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEBCIFLAY
Abies grandis (Grand 11r).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
NCBI_TaxiD=46611;
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                                                                                                                                                                                                                                                                                                 DB 10; Length
                                                                                                                                                                                                                                                                                               Query Match 68.3%; Score 2713.5; DB 10; Lengt
Best Local Similarity 66.9%; Pred. No. 2.1e-190;
Matches 500; Conservative 107; Mismatches 135; Indels
                                                                                                                                                                                                                                                                          853 AA; 98059 MW; 7ECB56123F12B8F1 CRC64;
                                                        SEQUENCE FROM N.A. MEDIAGE 11404343; MEDIAE 21297338; PubMed=11404343; Trapp S.C., Croteau R.B.; "Genomic organization of plant terpene synthases and
                                                                                                     evolutionary implications.";

Genetics 158:811-832(2001).

Genetics 158:811-832(2001).

GO, GO:0016829; F:1yase activity; IEA.

GO, GO:0008152; P:metabolism; IEA.

InterPro; IPR00130; Prenyltrans.

InterPro; IPR008949; Terpencid synth.

InterPro; IPR008949; Terpencid synth.

InterPro; IPR008949; Terpencid synth.

InterPro; IPR008949; Terpencid synth.

InterPro; IPR008949; Terpencid synth.

InterPro; IPR008949; Terpencid synth.

Pfam; PF00432; prenyltrans; 1.

Pfam; PF00432; prenyltrans; 1.

Pfam; PF01397; Terpenc_synth; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 LATLSCVLVLLKWAVGDLQVEQGIEFIKSNLELVKDETDQDSLVTDFEIIFPSLLREAQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGLDLPYHLPFISQIHQKRQKKLOKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQSR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGSPLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 GDGESMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIQSHFLLSDRL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98284004; PubMed=9618485; Bohlmann J., Crock J., Jetter R., Croteau R.; Bohlmann J., Crock J., Jetter R., Croteau R.; and Expendid-based defenses in conifers: cDNA cloning, characterization, and functional expression of wound-inducible (B)-alpha-bisabolene synthase from grand fir (Abies grandis)."; Proc. Natl. Acad. Sci. U.S.A. 95:6756-6761(1998).
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                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
E-alpha-bisabolene synthase (Fragment).
Abise grandis (Grand fir).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
NCIL_TAXID=46611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%; Score 2050.5; DB 10; Length 782; ilarity 50.8%; Pred. No. 8.9e-142; Conservative 152; Mismatches 206; Indels 9;
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               303 NFRDEKGDFFCFAGOTQIGVTDNLNLYRCSQVCFPGEKIMEEAKTFTTNHLQNALAKNNA 362
                                                                                                                                                                                                              RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNT 542
                                                                                                                                                                                                                                                                                                                                                                                           543 VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                          603 TVVLNSI-PFTGELLPDYILQQVDL--RSKFLHLVSLTGRLINDTKTYQAERNRGELVSS 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660 VQCYMRENPECTEEEALSHVYGIIDNALKELNWELANPASNAPLCVRRLLFNTARVMQLF 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 FDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQFGSNDVWLGKTVYKMLYVSNEKY
                                                                                                                                                                                                                                                             LELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFAAC
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X Trapp S.C., Croteau R.B.;

Trapp S.C., Croteau R.B.;

"Genomic organization of plant terpene synthases and molecular evolutionary implications.";

Genetics 158:811-232(201).

In Genetics 158:811-232(201).

GO: GO:0016829; F:1yase activity; IEA.

GO; GO:0016829; F:1yase activity.

R GO; GO:0016829; F:1yase activity.

Interpro; IPR008949; Terpene Synth C.

Interpro; IPR008949; Terpene Synth C.

Interpro; IPR008949; Terpene Synth C.

Interpro; IPR008930; Terpene Synth C.

Interpro; IPR001906; Terp_synth-like.

Pfam; PF01397; Terpene_synth-like.

Pfam; PF01397; Terpene_synth-C: 1.
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Abies.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
E-alpha-bisabolene synthase (Fragment).
Abies grandis (Grand fir).
Abies grandis (Grand fir).
Spermatophyta; Viridiplantes; Streptophyta; Embryophyta; Spermatophyta; Coniferales; Pinaceae; NUBI_TAXID=46611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               816 AA
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790 FKDGDGFGVSKLEVKDHIKECLIEPL
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                                                                                                                                VNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAKYVPTFNEYVENAKVSIALA 602
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MEDLINE=98284004; PubMed=9618485;

MEDLINE=98284004; PubMed=9618485;

Bohlmann J., Crock J., Jetter R., Croteau R.;

"Texpenoid-based defenses in conifers: cDNA cloning, characterization, and functional expression of wound-inducible (E)-alpha-bisabolene synthase from grand fir (Ables grandis).";

Proc. Natl. Acad. Sci. U.S.A. 95:6756-6761(1998).

EMBL: AP006195; ARC24192.1; -.
                                                                                                                                                   LINTLACLLTLKI WINGOI QVQKGVEFVRKHMEEMKDEAD-NHRPSGFEVVFPAMLDEAKS
LELAKLDFNMVQALHQKETQHIVSWWRESGFNDLTFTRQRPVEMYFSVAVSMFEPEFAAC
                                                                RIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFLGLYNT
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E-alpha-bisabolene synthase.
Abies grandis (Grand fir).
Eukaryota; Viridiplanes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR008509; Terpene synth.C.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008930; Terperorie proid.
InterPro; IPR001906; Terp synth.like.
Pfam; PP01397; Terpene synth, C;
Pfam; PP013976; Terpene synth, C;
SEQUENCE 817 AA; 93749 MW; 95FB06DBC
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Eukaryoch, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Eupatorieae; Stevia.
VCDI_TaxID=55670;
                                                                                                                                                  DGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVERLG
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MEDLINE=99435880; PubMed=10504563;

Richman A.S., Gijzen M., Starratt A.N., Yang Z., Brandle J.E.;
Richman A.S., Gijzen M., Starratt A.N., Yang Z., Brandle J.E.;
"Diterpene synthesis in Stevia rebaudiana: recruitment and up-
regulation of key enzymes from the gibberellin biosynthetic pathway.";

Regulation of key enzymes from the gibberellin biosynthetic pathway.";

Regulation of key enzymes from the gibberellin biosynthetic pathway.";

Regulation of key enzymes from the gibberellin biosynthetic pathway.";

Regulation of key enzymes from the gibberellin biosynthetic pathway.";

Responsible from the gibberellin biosynthetic pathway.";

Richerro; PRRO0530; Terpene synth C.

Richerro; PRR00830; Terpene synth.

Richerro; PRR00830; Terpene synth.

Richerro; PR001906; Terp synth. 1.

Refam; PR01397; Terpene synth, 1.

Refam; PR01397; Terpene synth, 1.

Refam; PR013936; Terpene synth, 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGI DRYFKKEI KESLDYVYRYWDAERGVGWARCNPI PDVDDTAMGLRI LRLHGYNVSSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENFRDEKGDPPCPAGQTQIGVTDNLNLYRCSQVCPPGEKIMBEAKTPTTNHLQNALAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MFQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRVLNTLACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDEADNHRPSGFEVVFPAMLDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAFDKWAVKKOLPGEVBYAIKYPWHRSMPRLEARSYIEQP-GSNDVWLGKTVYKMLYVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAACRIAYAKTSCLAVILDDLYD-THGSLDDLKLFSEAVRRWDISVLDSVRDNQLKVCFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKBAEWSAAKYVPTFNEYVENAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                   C; 1.
. 224575732606DCA1 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.8%; Score 1382; DB 10; Best Local Similarity 42.7%; Pred. No. 1.1e-92; Matches 280; Conservative 122; Mismatches 235;
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712 TARVMQLFY-MYRDGFGISDKEMKDHVSRTLFDPV
                                                 772 VAK--SPYYSAYCD-----DRTINFHIAKVLFERV
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                                                                                                                829
731 QVGMLTFSEE--IEGDMQQLAELVLSH-
                                                                                                                                        Created)
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Pfam; PF03936; Terpene synth C; 1
SEQUENCE 829 AA; 96226 MW; 3C
                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                PRELIMINARY;
                                                                                                                                                                            Copalyl diphosphate
                                                                                                                                                                                                                                                                  NCBI_TaxID=107238;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                       Croton sublyratus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSLGLDLPYHLPFISQIHQKRQKKQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ 180
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                       Lycopersicon esculentum (Tomato).
Bukaryota; Viridijlantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiida; Solanales; Solanaceae; Solanum.
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DRVINTLACVIALKSWNLHPDKILLGMSFMRENLSRIGDENAEHMPIGFEVAFPSLIEIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 QLLDKWIITKOLPGEVGYALDVPWYASLPRLETRFPLEHYGGEDDVWIGKTLYRMPLVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDTVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 SLYLELAKSDYNNCOALHOFEWRRIRKWYYECGLREFGLSEKRLLVTYYLGSASIFEAQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |:| | ::| | ::| STERWAWVKT----AALMDCVRSCFGSPQVSAAAFLCEFAHYSSTALNSRYNTEDRLVGVI
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                             34.6%; Score 1373; DB 10; Length 800; 39.5%; Pred. No. 5.2e-92;
                                                                                                                          Tomato cDNA for copalyl diphosphate synthase.";
Submitted (UUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO11677; BAA84918.1,
GO, GO:0016829; F:1yase activity; IEA.
GO, GO:001821; F:metabolism; IEA.
InterPro; IPR005630; Terpene synth.C.
InterPro; IPR008949; Terpened synth.C.
InterPro; IPR008930; Terp.Cyc.toroid.
InterPro; IPR008930; Terp.Synth.like.
Pfam; PP03393; Terpene synth,1.
Pfam; PP03393; Terpene synth,1.
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91698_MW;
 Copalyl diphosphate synthase
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                    SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=4081;
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--SDASELDANIKDTFLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Malpighiales, Euphorbiaceae, Crotonoideae, Crotoneae;
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"Copalyl diphosphate synthase from Croton sublyratus.";
"Copalyl diphosphate synthase from Croton sublyratus.";
Submitted (WAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 38040424; BA495612.1, -
GO, GO.001639; F:lyase activity; IEA.
GO, GO.0008152; P:metabolism; IEA.
InterPro; IPR008530; Terpene synth.
InterPro; IPR008930; Terpenold synth.
InterPro; IPR008930; Terpenold synth.
InterPro; IPR008930; Terp_GYC_foroid.
InterPro; IPR001906; Terp_Synth-like.
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3C3D00C6A848EFOA CRC64;
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Last annotation update)
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ALERLAWAKTAILMETIETILKDNSSQE-----SGNVLSSMNPNLMAAACM--
                                                                                         LENFRDEKGDPFCPAGOTOIGVTDNLNLYRCSQVCPPGEKIMEEAKTFTTNHLQNALAKN
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAINS-C. COlumbia;
G. 18 Bastide M., Gnoj L., Habermann K., Huang B.N., Gottesman T.,
Kaplan N., Lodhi M., Jensen K., Hameed A., Schutz K., Martienssen
Debhia N., Parnell L.D., McCombie W.R.,
"Arabidosis thaliana BAC TSJ8 from chromosome IV, short arm.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ENT-KAURENE Synthetase A.
GAI OR T5J8.9 OR AT4G02780.
Arabidopsis thaliana (Mouse-ear cress).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Plantaginaceae; Gratioleae; Scoparia.
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A SILthithaworn W., Sankawa U.;

SILthithaworn W., Sankawa U.;

A SILthithaworn W., Sankawa U.;

SILTHITHAWORN W., Sankawa U.;

A SILTHITHAWORN W., Sankawa U.;

A SILTHITHAWORN W., Sankawa U.;

AL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 799;
                                                                                                                                                                                                                                                                                                                       Toyomagu T., Miteuhashi W., Kamiya Y.;
"Gibberellin biosynthetic enzyme.";
"Gibberellin biosynthetic enzyme.";
"Gibberellin biosynthetic enzyme.";
"Gibberellin biosynthetic enzyme.";
"Gibberellin biosynthetic enzyme.";
"Gibberellin biosynthetic enzyme.";
"Go, Go:000152; PaBla40.1; -.
"Go, Go:000152; P:metabolism; IEA.
InterPro; IPR00830; Terpene synth."C.
InterPro; IPR00830; Terpenoid synth.
InterPro; IPR00830; Terpenoid synth.
InterPro; IPR001906; Terp. synth.like.
Pfam; PF01397; Terpene synth.like.
Pfam; PF01397; Terpene synth.c: 1.
SEQUENCE 799 AA; 91865 MM; 51940A6553B40BAS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Copalyldiphosphate synthase No1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
33.0%; Score 1309; DB 10;
Best Local Similarity 42.4%; Pred. No. 2.6e-87;
Matches 266; Conservative 118; Mismatches 216;
                                     Ź
                                     799
                                     PRT;
                                                                                                                                                              Lactuca sativa (Garden lettuce)
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Grand Rapids;
                                                                                                                                                                                                                                                    NCBI_TaxID=4236;
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                                   Q9FXV9
                                                                                                                                               LSCPS1
   RESULT 12
Q9FXV9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDVVDWQEITNLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENFRDEKGDFFCFAGQTQIGVTDNLNLYRCSQVCFPGEKIMBEAKTFTTNHLQNALAKN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SVRDNQLKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSVQASRLAGVLIG---TLNQMSFDLFMSHGRDVNNLLYLSW------GDW---- 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 YVPTFNEYVENAKVSIALATVVL---NSI--FFTGELLPDYILQQVDLRSKFLHLVSLTG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLINDTKTYQAERNRGELVSSVQCYMRENPECTEEBALSHVYGIIDNALKELNWELANPA 698
                                                                                                                                                                                                                                                                                                                                                                                      DRVLNTLACLLTLKIWNKGDIQVQKGVEFVRKHMEEMKDBADNHRPSGFEVVFPAMLDEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||::|||||::|||||DRLINTLACVVALRSWNLFPPHQCNKGITFFRENIGKLEDENDEHWFIGFEVAFPSLLEIA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGIDRY FXKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVSSDV
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                                                                                                                                                                                                                                                                                                                                                                 1 MFQSMGDGETNPSAYDTAWVARIPSIDGSGAPQFPQTLQWILNNQLPDGSWGEECIFLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACRIAYAKTSCLAVILDDLYDTHGSLDDLKLFSEA-----VRRWDISVLD-----
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 33.2%; Score 1320; DB 10; Length 802; al Similarity 36.6%; Pred. No. 4.1e-88; 281; Conservative 144; Mismatches 252; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNAPLCVRRLLFNTARVMQLFYMYRDGFGISDKEMKDHVSRTLFDPV 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U11034; AAA53632.1;
EMBL; AC004044, AAD536334.1;
EMBL; AC004044, AAD53334.1;
EMBL; AC004044; AAD15334.1;
EMBL; AC004045; CAB77763.1;
EMBL; AC0016829; F11yase activity; IEA.
GO; GO:001829; F11yase activity; IEA.
GO; GO:001829; F11yase activity; IEA.
InterPro; IPR005630; Terpene synth_C.
InterPro; IPR008309; Terpenoid synth.
InterPro; IPR008309; Terpenoid synth.
InterPro; IPR001906; Terpene synth, 1.
PEam; PF01397; Terpene synth, 1.
PEAM; PF013936; Terpene synth, 1.
                                                                                                                                                                                                                                        C; 1.
B2815AB0C06414F6 CRC64;
                                                                                                                                                                                                                                        36; Terpene_synth_C
802 AA; 93013 MW;
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Best Local Similarity
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                          632 WHGLMVALKGTLHEIALDVLMTHRRDIHPQLHHAWEMMLMRWQQGVDATEGQAELIVQTI 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEVPKNF-EKDGEFVCIAGOSTQAVTGMFNLYRASDQVMFPGEKILEDAKQFSYKFLREK 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKSLGLDLPYHLPFISQIHQKRQKKLQKIPLNVLHNHQTALLYSLEGLQDV--VDWQEIT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 VERLGIDRYFKKBIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
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LKVCFLGLYNTVNGFGKDGLKEQGRDVLGYLRKVWEGLLASYTK---EAEWSAAKYVPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 NLQSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDRVLNTLACLLTLKIWNKGDIQVQKGVBFVRKHMEEMKDEADNHRPSGFEVVFPAMLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPQSMGDGETNPSAYDTAWVARIPSI-DGSGAPQPPQTLQWILNNQLPDGSWGBECIFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] SEQUENCE FROM N.A. MEDLINE=99063778; PubMed=9847116; Smith M.W., Yamaguchi S., Ait-Ali T., Kamiya Y.; Smith M.W., Yamaguchi S., Ait-Ali T., Kamiya Y.; The first step of gibberellin biosynchesis in pumpkin is catalyzed the least two copallyl diphosphate synthases encoded by differentially regulated genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Cucurbitales, Cucurbitaceae, Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.6%; Score 1296.5; DB 10; Length 823; larity 38.3%; Pred. No. 2.2e-86; Conservative 135; Mismatches 271; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3F367AAF474721F7 CRC64;
                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                       823 AA
                                                                                                                                                                                                                                                                                                                                            Copalyl diphosphate synthase 1.
Cucurbita maxima (Pumpkin) (Winter squash)
                                                                                   589 N----EYVEN---AKVSIALATVVLNSI 609
                                                                                                       | :| :| : | : | : | 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF049905; AAD04292.1; --
EMBL; AF049905; AAD04292.1; --
GO; GO:0016829; F:1yase activity; IEA.
GO; GO:000152; P:metabolism; IEA.
InterPro; IPR005630; Terpenoid synth.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR001906; Terp coroid.
InterPro; IPR001906; Terp synth.like.
Pfam; PF01397; Terpene_synth; 1.
Proventy PF03395; Terpene_synth; 1.
                                                                                                                                                                                                                                     PRT,
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532
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Matches
                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                 531 ---QLKVCFLG----LYNTVNGFGXDGLKEQGRDVLGYLRKVWEGLLASYTKEAEWSAAK
                                 638 GNVQQKGGGQGLVGILLRTLTSISLDILVSHGPDITHHLHQAWEKWLFKWQEDGD----
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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"Cucurbita maxima mRNA for copalyl diphosphate synthase 1,
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RMBL; AB109763; BAC76429.1; -..

GO; GO:0016829; F:1yase activity; IEA.

GO; GO:0018152; P:metabolism; IEA.

InterPro; IPR008949; Terpene synth.

InterPro; IPR008949; Terpeneld synth.

InterPro; IPR008949; Terpeneld synth.

InterPro; IPR001906; Terp_synth-like.

Rem; PR01397; Terpene synth; 1.

Rem; PR03936; Terpene synth; 1.

Rem; PR03936; Terpene synth; 1.

Rem; PR0396; Terpene synth; 1.

Rem; PR0396; Terpene synth; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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             SDVLENFRDEKGDFFCFAGQTQIGVTDNLNLYRCS-QVCFPGEKIMEEAKTFTTNHLQNA
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NLOSRDGSFLSSPASTACVFMHTQNKRCLHFLNFVLSKFGDYVPCHYPLDLFERLWAVDT
                                                   VERLGIDRY FKKEIKESLDYVYRYWDAERGVGWARCNPIPDVDDTAMGLRILRLHGYNVS
                                                                                                                                                           LAKNNAPDKWAVKKDLPGEVEYAIKYPWHRSMPRLEARSYIEQF-GSNDVWLGKTVYKML
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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MEDLINE=95210929; PubMed=7696880;
Bensen R.J., Johal G.S., Crane V.C., Tossberg J.T., Schnable I
Meeley R.B., Briggs S.P.;
"Cloning and characterization of the maize Anl gene.";
Plant Cell 7.75-84(1995).

PIR: 1702959; T02959.
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR005630; Terpene synth C.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008949; Terpenoid synth.
InterPro; IPR008930; Terperoid synth.
Fefam; PF01397; Terpene synth.
Ffam; PF01397; Terpene synth. C; 1.
SEQUENCE 823 AA; 95123 MW; E4D9C97CD
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
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                                                1 MFQSMGDGETNPSAYDTAWVARIPSI -- DGSGAPQFPQTLQWILNNQLPDGSWGEECIFL
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            Best Local Similarity 36.5%; Pred. No. 3.7e-86; Matches 289; Conservative 146; Mismatches 243; Indels 113;
 Length 823;
 DB 10;
32.6%; Score 1293.5; 36.5%; Pred. No. 3.7e
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